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<110> Seishi KATO  
 Chikashi EGUCHI  
 Mihoro SAEKI

<120> Human Proteins and cDNAs thereof

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09890688-092701

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Arg Tyr Asn Arg Lys Arg Phe Phe Ala Leu Pro Tyr Val Asp His Phe  
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Val Val Ala Asn Gly Gly Leu Gly Asn Gly Val Ser Arg Asn Gln Leu  
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Asp Ser Gln Arg Lys Glu Thr Pro Pro Ser Phe Pro Glu Ser Asp Lys	
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Ile Ala Gly His Phe Ser Ser Thr Arg His Thr Pro Trp Pro His Ile	
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Leu	Trp	Thr	His	Gly	Ile	Thr	Cys	Arg	Lys	Phe	Asp	Thr	Val	Gln	Ala	290	295	300
Ser	Glu	Ser	Leu	Lys	Ser	Gly	Ile	Ile	Thr	Ser	Asp	Val	Gly	Asp	Leu	305	310	315
Thr	Leu	Ser	Lys	Arg	Gly	Leu	Arg	Thr	Ser	Phe	Thr	Phe	Arg	Lys	Val	325	330	335
Arg	Gln	Thr	Pro	Cys	Asn	Cys	Ser	Tyr	Pro	Leu	Val	Cys	Asp	Ser	Gln	340	345	350
Arg	Lys	Glu	Thr	Pro	Pro	Ser	Phe	Pro	Glu	Ser	Asp	Lys	Glu	Ala	Ser	355	360	365
Arg	Leu	Glu	Gln	Glu	Tyr	Val	His	Gln	Val	Tyr	Glu	Glu	Ile	Ala	Gly	370	375	380
His	Phe	Ser	Ser	Thr	Arg	His	Thr	Pro	Trp	Pro	His	Ile	Val	Glu	Phe	385	390	395
Leu	Lys	Ala	Leu	Pro	Ser	Gly	Ser	Ile	Val	Ala	Asp	Ile	Gly	Cys	Gly	405	410	415
Asn	Gly	Lys	Tyr	Leu	Gly	Ile	Asn	Lys	Glu	Leu	Tyr	Met	Glu	Arg	Arg	420	425	430





09890668-092701

25	30	35	
aag gag ctg ctg gga cag ggg att gat tat gag aag atc ctg aag ctc			197
Lys Glu Leu Leu Gly Gln Gly Ile Asp Tyr Glu Lys Ile Leu Lys Leu			
40	45	50	
acg gct gac gcc aag ttt gag tca ggc gat gtg aag gcc aca gtg gca			245
Thr Ala Asp Ala Lys Phe Glu Ser Gly Asp Val Lys Ala Thr Val Ala			
55	60	65	70
gtg ctg agt ttc atc ctc tcc agt gcg gcc aag cac agt gtc gat ggc			293
Val Leu Ser Phe Ile Leu Ser Ser Ala Ala Lys His Ser Val Asp Gly			
75	80	85	
gaa tcc ttg tcc agt gaa ctg cag cag ctg ggg ctg ccc aaa gag cac			341
Glu Ser Leu Ser Ser Glu Leu Gln Gln Leu Gly Leu Pro Lys Glu His			
90	95	100	
gcg gcc agc ctg tgc cgc tgt tat gag gag aag caa agc ccc ttg cag			389
Ala Ala Ser Leu Cys Arg Cys Tyr Glu Glu Lys Gln Ser Pro Leu Gln			
105	110	115	
aag cac ttg cgg gtc tgc agc cta cgc atg aat agg ttg gca ggt gtg			437
Lys His Leu Arg Val Cys Ser Leu Arg Met Asn Arg Leu Ala Gly Val			
120	125	130	
ggc tgg cgg gtg gac tac acc ctg agc tcc agc ctg ctg caa tcc gtg			485
Gly Trp Arg Val Asp Tyr Thr Leu Ser Ser Ser Leu Leu Gln Ser Val			
135	140	145	150
gaa gag ccc atg gtg cac ctg cgg ctg gag gtg gca gct gcc cca ggg			533
Glu Glu Pro Met Val His Leu Arg Leu Glu Val Ala Ala Ala Pro Gly			
155	160	165	
acc cca gcc cag cct gtt gcc atg tcc ctc tca gca gac aag ttc cag			581
Thr Pro Ala Gln Pro Val Ala Met Ser Leu Ser Ala Asp Lys Phe Gln			
170	175	180	
gtc ctc ctg gca gaa ctg aag cag gcc cag acc ctg atg agc tcc ctg			629
Val Leu Leu Ala Glu Leu Lys Gln Ala Gln Thr Leu Met Ser Ser Leu			
185	190	195	
ggc tga ggagaagggt gttccaggcc tgtgtggagc cgcctgccc gtatggagtc			685
Gly			
acgccctctg aactgctctt cgaggaggcag cccctggttct aggatgctga ggccctggcc			745
cggaactctgg cctcccagat cccagctgc ctcacttctc tcttgagaac ttggctcagg			805
gctcctgagg acctttccca gcattacctt cccttcctt gaaaggcaat tgttggtgt			865
tttcataagc aggaaaaata aacagaagta taaagg			901

<210> 20  
 <211> 199  
 <212> PRT

<213> Homo sapiens

<400> 20

Met Arg Phe Arg Phe Cys Gly Asp Leu Asp Cys Pro Asp Trp Val Leu  
1 5 10 15

Ala Glu Ile Ser Thr Leu Ala Lys Met Ser Ser Val Lys Leu Arg Leu  
20 25 30

Leu Cys Ser Gln Val Leu Lys Glu Leu Leu Gly Gln Gly Ile Asp Tyr  
35 40 45

Glu Lys Ile Leu Lys Leu Thr Ala Asp Ala Lys Phe Glu Ser Gly Asp  
50 55 60

Val Lys Ala Thr Val Ala Val Leu Ser Phe Ile Leu Ser Ser Ala Ala  
65 70 75 80

Lys His Ser Val Asp Gly Glu Ser Leu Ser Ser Glu Leu Gln Gln Leu  
85 90 95

Gly Leu Pro Lys Glu His Ala Ala Ser Leu Cys Arg Cys Tyr Glu Glu  
100 105 110

Lys Gln Ser Pro Leu Gln Lys His Leu Arg Val Cys Ser Leu Arg Met  
115 120 125

Asn Arg Leu Ala Gly Val Gly Trp Arg Val Asp Tyr Thr Leu Ser Ser  
130 135 140

Ser Leu Leu Gln Ser Val Glu Glu Pro Met Val His Leu Arg Leu Glu  
145 150 155 160

Val Ala Ala Ala Pro Gly Thr Pro Ala Gln Pro Val Ala Met Ser Leu  
165 170 175

Ser Ala Asp Lys Phe Gln Val Leu Leu Ala Glu Leu Lys Gln Ala Gln  
180 185 190

Thr Leu Met Ser Ser Leu Gly  
195

<210> 21

<211> 1274

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (131)..(1111)

<400> 21

acagcgcgtc gcggcagccc ccaaggaaga ccagcctgcc tctggtcggt tectggcgct 60

ctgcgttttcg tgaccttgct cagtagaagg ctatttaatt ttcacaactg cttgaatttt 120

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gacatacaag atg aag caa gat gcc tca aga aat gct gcc tac act gtg	169
Met Lys Gln Asp Ala Ser Arg Asn Ala Ala Tyr Thr Val	
1 5 10	
gat tgt gaa gat tat gtg cat gtg gta gaa ttt aat ccc ttt gag aat	217
Asp Cys Glu Asp Tyr Val His Val Val Glu Phe Asn Pro Phe Glu Asn	
15 20 25	
ggg gat tca gga aac cta att gca tat ggt ggc aat aat tat gtg gtc	265
Gly Asp Ser Gly Asn Leu Ile Ala Tyr Gly Gly Asn Asn Tyr Val Val	
30 35 40 45	
att ggc acg tgt acg ttt cag gaa gaa gaa gca gac gtt gaa ggc att	313
Ile Gly Thr Cys Thr Phe Gln Glu Glu Glu Ala Asp Val Glu Gly Ile	
50 55 60	
cag tat aaa aca ctt cga aca ttt cac cat gga gtc agg gtt gat ggc	361
Gln Tyr Lys Thr Leu Arg Thr Phe His His Gly Val Arg Val Asp Gly	
65 70 75	
ata gct tgg agc cca gag act aga ctt gat tca ttg cct cca gta atc	409
Ile Ala Trp Ser Pro Glu Thr Arg Leu Asp Ser Leu Pro Pro Val Ile	
80 85 90	
aaa ttt tgt act tca gct gct gat atg aaa att aga tta ttt act tca	457
Lys Phe Cys Thr Ser Ala Ala Asp Met Lys Ile Arg Leu Phe Thr Ser	
95 100 105	
gat ctt cag gat aaa aat gaa tat aag gtt tta gag ggc cat acc gat	505
Asp Leu Gln Asp Lys Asn Glu Tyr Lys Val Leu Glu Gly His Thr Asp	
110 115 120 125	
ttc att aat ggt ttg gtg ttt gat ccc aaa gaa ggc caa gaa att gca	553
Phe Ile Asn Gly Leu Val Phe Asp Pro Lys Glu Gly Gln Glu Ile Ala	
130 135 140	
agt gtg agt gac gat cac acc tgc agg att tgg aac ttg gaa gga gtg	601
Ser Val Ser Asp Asp His Thr Cys Arg Ile Trp Asn Leu Glu Gly Val	
145 150 155	
caa aca gct cat ttt gtt ctt cat tct cct ggc atg agt gtg tgc tgg	649
Gln Thr Ala His Phe Val Leu His Ser Pro Gly Met Ser Val Cys Trp	
160 165 170	
cat cct gag gag act ttt aag cta atg gtt gca gag aag aat gga aca	697
His Pro Glu Glu Thr Phe Lys Leu Met Val Ala Glu Lys Asn Gly Thr	
175 180 185	
atc cgg ttt tat gat ctt ttg gcc caa cag gct att tta tct ctt gaa	745
Ile Arg Phe Tyr Asp Leu Leu Ala Gln Gln Ala Ile Leu Ser Leu Glu	
190 195 200 205	
tca gaa caa gtg cca tta atg tca gca cac tgg tgc tta aaa aac acc	793
Ser Glu Gln Val Pro Leu Met Ser Ala His Trp Cys Leu Lys Asn Thr	
210 215 220	
ttc aaa gtt gga gcc gtt gca gga aat gat tgg tta att tgg gat att	841

Phe Lys Val Gly Ala Val Ala Gly Asn Asp Trp Leu Ile Trp Asp Ile  
 225 230 235

act cgg tcc agt tat cct caa aat aag aga cct gtt cac atg gat cga 889  
 Thr Arg Ser Ser Tyr Pro Gln Asn Lys Arg Pro Val His Met Asp Arg  
 240 245 250

gcc tgc tta ttc agg tgg tcc aca att agt gaa aat ctg ttt gca acc 937  
 Ala Cys Leu Phe Arg Trp Ser Thr Ile Ser Glu Asn Leu Phe Ala Thr  
 255 260 265

act ggt tat cct ggc aaa atg gca agc cag ttt caa att cat cat tta 985  
 Thr Gly Tyr Pro Gly Lys Met Ala Ser Gln Phe Gln Ile His His Leu  
 270 275 280 285

gga cac cct cag ccc atc ctc atg ggt tct gta gcc gtt gga tct gga 1033  
 Gly His Pro Gln Pro Ile Leu Met Gly Ser Val Ala Val Gly Ser Gly  
 290 295 300

ctg tcc tgg cat cga act ctc cct ctg tgt gta att gga gga gac cac 1081  
 Leu Ser Trp His Arg Thr Leu Pro Leu Cys Val Ile Gly Gly Asp His  
 305 310 315

aag ctg ttg ttt tgg gtg act gaa gta taa agtgttttct gtaccttaga 1131  
 Lys Leu Leu Phe Trp Val Thr Glu Val  
 320 325

ttcacaaact ttgtatTTTT agtacatatt ttgaagaatt tctatagtag atattttgaa 1191

gaatttttat atcaaatata ccgtatactt tagaaaatgt ctcagttgct tttattaaat 1251

aaaatgttga tggtttgaaa aat 1274

<210> 22

<211> 326

<212> PRT

<213> Homo sapiens

<400> 22

Met Lys Gln Asp Ala Ser Arg Asn Ala Ala Tyr Thr Val Asp Cys Glu  
 1 5 10 15

Asp Tyr Val His Val Val Glu Phe Asn Pro Phe Glu Asn Gly Asp Ser  
 20 25 30

Gly Asn Leu Ile Ala Tyr Gly Gly Asn Asn Tyr Val Val Ile Gly Thr  
 35 40 45

Cys Thr Phe Gln Glu Glu Glu Ala Asp Val Glu Gly Ile Gln Tyr Lys  
 50 55 60

Thr Leu Arg Thr Phe His His Gly Val Arg Val Asp Gly Ile Ala Trp  
 65 70 75 80

Ser Pro Glu Thr Arg Leu Asp Ser Leu Pro Pro Val Ile Lys Phe Cys  
 85 90 95

**SECRET**

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<220>  
<221> CDS  
<222> (33)..(185)
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29

cttttcgagg taggagtcga ctctgtgag gt atg gtg ctg ggt gca gat gca 53  
Met Val Leu Gly Ala Asp Ala  
1 5

gtg tgg ctc tgg ata gca cct tat gga cag ttg tgt ccc caa gga agg 101  
Val Trp Leu Trp Ile Ala Pro Tyr Gly Gln Leu Cys Pro Gln Gly Arg  
10 15 20

atg aga ata gct act gaa gtc cta aag agc aag cct aac tca agc cat 149  
Met Arg Ile Ala Thr Glu Val Leu Lys Ser Lys Pro Asn Ser Ser His  
25 30 35

tgg cac aca ggc att aga cag aaa gct gga agt tga aatggtggag 195  
Trp His Thr Gly Ile Arg Gln Lys Ala Gly Ser  
40 45 50

tccaacttgc ctggaccagc ttaatgggtc tgctcctggt aacgttttta tccatggatg 255

acttgcttgg gtaaggacat gaagacagtt cctgtcatac cttttaaagg tacatgtttt 315

attgatgtta acgttaattg attgagctac tgtagtgat gatttttaaaa ttaaagcaga 375

tgggaatctc tctgagaaag aaaatggaga ttaatcttaa actgaaacag tagttgggaa 435

atctttttaga aatccaccta ttactaccta ttggtaaagg agattaaatt tctacaggta 495

tggagagtgc gcttgactac actgtgtgga gcaagtttta aagaagcaaa ggactcagaa 555

ttcatgattg aagaaatgca ggcagacctg ttatcctaaa ctaggtgagt cagcttttgg 615

tacatgtgat gattttcagt gtaaccaatg atgtaatgat tctgccaaat gaaatataat 675

gatatcactg taaaaccgtt ccattttgat tctgaggta ctctactaac aagcatcaca 735

catttgtatt ttgccctgat taatatgttg gcttcgcttt cagggttttt aatgaccaca 795

acaagcaagc atgcagctta ctgcttgaaa gggctcttgcc tcaccaagc tagagtgcag 855

tggcctttga agcttactac agcctcaaac ttctgggctc aagtgatcct cagcctccca 915

gtggctcttg tagactgcct gatggagtct catggcacia gaagattaaa acagtgtctc 975

caattttaat aaatttttgc aatcc 1000

<210> 24  
<211> 50  
<212> PRT  
<213> Homo sapiens

<400> 24  
Met Val Leu Gly Ala Asp Ala Val Trp Leu Trp Ile Ala Pro Tyr Gly  
1 5 10 15

Gln Leu Cys Pro Gln Gly Arg Met Arg Ile Ala Thr Glu Val Leu Lys  
20 25 30

Ser Lys Pro Asn Ser Ser His Trp His Thr Gly Ile Arg Gln Lys Ala  
 35 40 45

Gly Ser  
 50

<210> 25

<211> 1087

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (28)..(558)

<400> 25

agcttcgagg tttcctgggc tactacg atg gcg atg agt ttc gag tgg ccg tgg 54  
 Met Ala Met Ser Phe Glu Trp Pro Trp  
 1 5

cag tat cgc ttc cca ccc ttc ttt acg tta caa ccg aat gtg gac act 102  
 Gln Tyr Arg Phe Pro Pro Phe Phe Thr Leu Gln Pro Asn Val Asp Thr  
 10 15 20 25

cgg cag aag cag ctg gcc gcc tgg tgc tcg ctg gtc ctg tcc ttc tgc 150  
 Arg Gln Lys Gln Leu Ala Ala Trp Cys Ser Leu Val Leu Ser Phe Cys  
 30 35 40

cgc ctg cac aaa cag tcc agc atg acg gtg atg gaa gct cag gag agc 198  
 Arg Leu His Lys Gln Ser Ser Met Thr Val Met Glu Ala Gln Glu Ser  
 45 50 55

ccg ctc ttc aac aac gtc aag cta cag cga aag ctt cct gtg gag tcg 246  
 Pro Leu Phe Asn Asn Val Lys Leu Gln Arg Lys Leu Pro Val Glu Ser  
 60 65 70

atc cag att gta tta gag gaa ctg agg aag aaa ggg aac ctc gag tgg 294  
 Ile Gln Ile Val Leu Glu Glu Leu Arg Lys Lys Gly Asn Leu Glu Trp  
 75 80 85

ttg gat aag agc aag tcc agc ttc ctg atc atg tgg cgg agg cca gaa 342  
 Leu Asp Lys Ser Lys Ser Ser Phe Leu Ile Met Trp Arg Arg Pro Glu  
 90 95 100 105

gaa tgg ggg aaa ctc atc tat cag tgg gtt tcc agg agt ggc cag aac 390  
 Glu Trp Gly Lys Leu Ile Tyr Gln Trp Val Ser Arg Ser Gly Gln Asn  
 110 115 120

aac tcc gtc ttt acc ctg tat gaa ctg act aat ggg gaa gac aca gag 438  
 Asn Ser Val Phe Thr Leu Tyr Glu Leu Thr Asn Gly Glu Asp Thr Glu  
 125 130 135

gat gag gag ttc cac ggg ctg gat gaa gcc act cta ctg cgg gct ctg 486  
 Asp Glu Glu Phe His Gly Leu Asp Glu Ala Thr Leu Leu Arg Ala Leu  
 140 145 150

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cag gcc cta cag cag gag cac aag gcc gag atc atc act gtc agc gat 534  
Gln Ala Leu Gln Gln Glu His Lys Ala Glu Ile Ile Thr Val Ser Asp  
155 160 165

ggc cga ggc gtc aag ttc ttc tag cagggacctg tctcccttta cttcttacct 588  
Gly Arg Gly Val Lys Phe Phe  
170 175

cccacctttc cagggctttc aaaaggagac agaccacagt tccccaaaag actggatctg 648  
tgactccacc agactcaaaa ggactccagt cctgaaggct gggacctggg gatgggtttc 708  
tcacacccca tatgtctgtc ctttgatag ggtgaggctg aagcaccagg gagaaaatat 768  
gtgcttcttc tcgcctacc tcctttccca tcttagactg tccttgagcc agggctctgta 828  
aacctgacac tttatatgtg ttcacacatg taagtacata cacacatgcy cctgcagcac 888  
atgcttctgt ctctcctcc tcccaccct ttagctgctg ttgcctccct tctcaggctg 948  
gtgctggatc cttcctaggg gatgggggaa gccctggctg caggcagcct tccaggcaat 1008  
atgaagatag gaggccacg ggcctggcag tgagaggtgt ggccccacac cgatttatga 1068  
tattaaaatc tcaactccc 1087

<210> 26  
<211> 176  
<212> PRT  
<213> Homo sapiens

<400> 26  
Met Ala Met Ser Phe Glu Trp Pro Trp Gln Tyr Arg Phe Pro Pro Phe  
1 5 10 15  
Phe Thr Leu Gln Pro Asn Val Asp Thr Arg Gln Lys Gln Leu Ala Ala  
20 25 30  
Trp Cys Ser Leu Val Leu Ser Phe Cys Arg Leu His Lys Gln Ser Ser  
35 40 45  
Met Thr Val Met Glu Ala Gln Glu Ser Pro Leu Phe Asn Asn Val Lys  
50 55 60  
Leu Gln Arg Lys Leu Pro Val Glu Ser Ile Gln Ile Val Leu Glu Glu  
65 70 75 80  
Leu Arg Lys Lys Gly Asn Leu Glu Trp Leu Asp Lys Ser Lys Ser Ser  
85 90 95  
Phe Leu Ile Met Trp Arg Arg Pro Glu Glu Trp Gly Lys Leu Ile Tyr  
100 105 110  
Gln Trp Val Ser Arg Ser Gly Gln Asn Asn Ser Val Phe Thr Leu Tyr  
115 120 125



Glu Leu Thr Asn Gly Glu Asp Thr Glu Asp Glu Glu Phe His Gly Leu  
130 135 140

Asp Glu Ala Thr Leu Leu Arg Ala Leu Gln Ala Leu Gln Gln Glu His  
145 150 155 160

Lys Ala Glu Ile Ile Thr Val Ser Asp Gly Arg Gly Val Lys Phe Phe  
165 170 175

<210> 27  
<211> 703  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (67)..(222)

<400> 27  
cgggcgcgag gcggccaccg tggagagcag agcgcggcgg ctggaagctg ctaagtcaga 60  
gccgcg atg ttc cgg att gag ggc ctc gcg ccg aag ctg gac ccg gag 108  
Met Phe Arg Ile Glu Gly Leu Ala Pro Lys Leu Asp Pro Glu  
1 5 10  
gag atg aaa cgg aag atg cgc gag gat gtg atc tcc tcc ata cgg aac 156  
Glu Met Lys Arg Lys Met Arg Glu Asp Val Ile Ser Ser Ile Arg Asn  
15 20 25 30  
ttt ctc atc tac gtg gcc ctc ctg cga gtc act cca ttt atc tta aag 204  
Phe Leu Ile Tyr Val Ala Leu Leu Arg Val Thr Pro Phe Ile Leu Lys  
35 40 45  
aaa ttg gac agc ata tga agacaggaca tcacatatga atgcacgata 252  
Lys Leu Asp Ser Ile  
50

tgaagagcct gggttacagtt tcgactcctc tctgcaagtg aataggccca gaaaggtgta 312  
agagactcct tgaatggaca taaaattctg cttgttaaga acaagtttg ctctggtaac 372  
tgaccttcaa agctaaaata taaaactatt tgggaagtat gaaacgatgt ctctgatct 432  
ggtgtaccct tatccctgtg acgtttggcc cctgacaata ctggtataat tgtaaataat 492  
gtcaaaactcc gttttctagc aagtattaag ggagctgtgt ctgaaatggc actgtcttgt 552  
cagtcatttc tgtttacctt tttcttctgc ccagagtgt tttgtgaaga gtctcttata 612  
ttatgttttg tggaaatcag cacacaacca caatgacatt taagcacagg atcattatta 672  
gtctatgttt ttaataaaca tatcaattaa g 703

<210> 28  
<211> 51

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<212> PRT

<213> Homo sapiens

<400> 28

Met Phe Arg Ile Glu Gly Leu Ala Pro Lys Leu Asp Pro Glu Glu Met  
1 5 10 15

Lys Arg Lys Met Arg Glu Asp Val Ile Ser Ser Ile Arg Asn Phe Leu  
20 25 30

Ile Tyr Val Ala Leu Leu Arg Val Thr Pro Phe Ile Leu Lys Lys Leu  
35 40 45

Asp Ser Ile  
50

<210> 29

<211> 921

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (204)..(776)

<400> 29

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actttgagcc tttttagtgc ctgatgaata atttcatttt cctcaagttt atgacactcg 120

gaacgtcaag aactggaggt ttgtgcaatt tgagaccggt cggcactgtg cagagatcag 180

agtactaaga gacagagatt aaa atg gct tcc aga gga aag aca gag aca agc 233

Met Ala Ser Arg Gly Lys Thr Glu Thr Ser  
1 5 10

aaa tta aag cag aat tta gaa gaa cag ttg gat aga ctc atg caa caa 281

Lys Leu Lys Gln Asn Leu Glu Glu Gln Leu Asp Arg Leu Met Gln Gln  
15 20 25

tta caa gat ctg gag gaa tgc aga gag gaa ctt gat aca gat gaa tat 329

Leu Gln Asp Leu Glu Glu Cys Arg Glu Glu Leu Asp Thr Asp Glu Tyr  
30 35 40

gaa gaa acc aaa aag gaa act ctg gag caa cta agt gaa ttt aat gat 377

Glu Glu Thr Lys Lys Glu Thr Leu Glu Gln Leu Ser Glu Phe Asn Asp  
45 50 55

tca cta aag aaa att atg tct gga aat atg act ttg gta gat gaa cta 425

Ser Leu Lys Lys Ile Met Ser Gly Asn Met Thr Leu Val Asp Glu Leu  
60 65 70

agt gga atg cag ctg gct att cag gca gct atc agc cag gcc ttt aaa 473

Ser Gly Met Gln Leu Ala Ile Gln Ala Ala Ile Ser Gln Ala Phe Lys  
75 80 85 90

09890688.092704

acc cca gag gtc atc aga ttg ttt gca aag aaa caa cca ggt cag ctt 521  
Thr Pro Glu Val Ile Arg Leu Phe Ala Lys Lys Gln Pro Gly Gln Leu  
95 100 105

cgg aca agg tta gca gag atg gat aga gat ctg atg gta gga aag ctg 569  
Arg Thr Arg Leu Ala Glu Met Asp Arg Asp Leu Met Val Gly Lys Leu  
110 115 120

gaa aga gac ctg tac act caa cag aaa gtg gag ata cta aca gct ctt 617  
Glu Arg Asp Leu Tyr Thr Gln Gln Lys Val Glu Ile Leu Thr Ala Leu  
125 130 135

agg aaa ctt gga gag aag ctg act gca gat gat gag gcc ttc ttg tca 665  
Arg Lys Leu Gly Glu Lys Leu Thr Ala Asp Asp Glu Ala Phe Leu Ser  
140 145 150

gca aat gca ggt gct ata ctc agc cag ttt gag aaa gtc tct aca gac 713  
Ala Asn Ala Gly Ala Ile Leu Ser Gln Phe Glu Lys Val Ser Thr Asp  
155 160 165 170

ctt ggc tct gga gac aaa att ctt gct ctg gca agt ttt gag gtt gaa 761  
Leu Gly Ser Gly Asp Lys Ile Leu Ala Leu Ala Ser Phe Glu Val Glu  
175 180 185

aaa aca aaa aaa tga catggtgcag aagcttgtaa cattgatcac attcttaatg 816  
Lys Thr Lys Lys  
190

taaatggtgt ctttcttctg ggggttttcag ttattgcaaa gaaatgaaga gattctggaa 876

atgcatcaat aacctaagaa aaagcgacat aaaaatatac ttatg 921

<210> 30  
<211> 190  
<212> PRT  
<213> Homo sapiens

<400> 30  
Met Ala Ser Arg Gly Lys Thr Glu Thr Ser Lys Leu Lys Gln Asn Leu  
1 5 10 15

Glu Glu Gln Leu Asp Arg Leu Met Gln Gln Leu Gln Asp Leu Glu Glu  
20 25 30

Cys Arg Glu Glu Leu Asp Thr Asp Glu Tyr Glu Glu Thr Lys Lys Glu  
35 40 45

Thr Leu Glu Gln Leu Ser Glu Phe Asn Asp Ser Leu Lys Lys Ile Met  
50 55 60

Ser Gly Asn Met Thr Leu Val Asp Glu Leu Ser Gly Met Gln Leu Ala  
65 70 75 80

Ile Gln Ala Ala Ile Ser Gln Ala Phe Lys Thr Pro Glu Val Ile Arg  
85 90 95

09890688-092701

Leu Phe Ala Lys Lys Gln Pro Gly Gln Leu Arg Thr Arg Leu Ala Glu  
 100 105 110  
 Met Asp Arg Asp Leu Met Val Gly Lys Leu Glu Arg Asp Leu Tyr Thr  
 115 120 125  
 Gln Gln Lys Val Glu Ile Leu Thr Ala Leu Arg Lys Leu Gly Glu Lys  
 130 135 140  
 Leu Thr Ala Asp Asp Glu Ala Phe Leu Ser Ala Asn Ala Gly Ala Ile  
 145 150 155 160  
 Leu Ser Gln Phe Glu Lys Val Ser Thr Asp Leu Gly Ser Gly Asp Lys  
 165 170 175  
 Ile Leu Ala Leu Ala Ser Phe Glu Val Glu Lys Thr Lys Lys  
 180 185 190

<210> 31  
 <211> 584  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (41)..(418)

<400> 31  
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 Met Lys Leu Leu Thr  
 1 5  
 cac aat ctg ctg agc tcg cat gtg cgg ggg gtg ggg tcc cgt ggc ttc 103  
 His Asn Leu Leu Ser Ser His Val Arg Gly Val Gly Ser Arg Gly Phe  
 10 15 20  
 ccc ctg cgc ctc cag gcc acc gag gtc cgt atc tgc cct gtg gaa ttc 151  
 Pro Leu Arg Leu Gln Ala Thr Glu Val Arg Ile Cys Pro Val Glu Phe  
 25 30 35  
 aac ccc aac ttc gtg gcg cgt atg ata cct aaa gtg gag tgg tcg gcg 199  
 Asn Pro Asn Phe Val Ala Arg Met Ile Pro Lys Val Glu Trp Ser Ala  
 40 45 50  
 ttc ctg gag gcg gcc gat aac ttg cgt ctg atc cag gtg ccg aaa ggg 247  
 Phe Leu Glu Ala Ala Asp Asn Leu Arg Leu Ile Gln Val Pro Lys Gly  
 55 60 65  
 ccg gtt gag gga tat gag gag aat gag gag ttt ctg agg acc atg cac 295  
 Pro Val Glu Gly Tyr Glu Glu Asn Glu Glu Phe Leu Arg Thr Met His  
 70 75 80 85  
 cac ctg ctg ctg gag gtg gaa gtg ata gag ggc acc ctg cag tgc ccg 343  
 His Leu Leu Leu Glu Val Glu Val Ile Glu Gly Thr Leu Gln Cys Pro  
 90 95 100

gaa tct gga cgt atg ttc ccc atc agc cgc ggg atc ccc aac atg ctg 391  
Glu Ser Gly Arg Met Phe Pro Ile Ser Arg Gly Ile Pro Asn Met Leu  
105 110 115

ctg agt gaa gag gaa act gag agt tga ttgtgccagg cgccagtttt 438  
Leu Ser Glu Glu Glu Thr Glu Ser  
120 125

tcttgttatg actgtgtatt tttgttgatc tataccctgt ttccgaattc tgccgtgtgt 498

atccccaacc cttgacccaa tgacaccaaa cacagtgttt ttgagctcgg tattatatat 558

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<211> 125

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<213> Homo sapiens

<400> 32

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Cys Pro Val Glu Phe Asn Pro Asn Phe Val Ala Arg Met Ile Pro Lys  
35 40 45

Val Glu Trp Ser Ala Phe Leu Glu Ala Ala Asp Asn Leu Arg Leu Ile  
50 55 60

Gln Val Pro Lys Gly Pro Val Glu Gly Tyr Glu Glu Asn Glu Glu Phe  
65 70 75 80

Leu Arg Thr Met His His Leu Leu Leu Glu Val Glu Val Ile Glu Gly  
85 90 95

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<211> 875

<212> DNA

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<222> (25)..(555)

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Pro	Gln	Gly	Arg	Glu	Ala	Pro	Gly	Pro	Ala	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly		
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agc	cgt	tgg	gct	gag	tcg	gga	tcg	ggg	acg	tcg	ccc	gag	agc	ggg	gac				147
Ser	Arg	Trp	Ala	Glu	Ser	Gly	Ser	Gly	Thr	Ser	Pro	Glu	Ser	Gly	Asp				
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gag	gag	gtg	tcg	ggc	gcg	ggt	tcg	agc	ccg	gtg	tcg	ggc	ggc	gtg	aac				195
Glu	Glu	Val	Ser	Gly	Ala	Gly	Ser	Ser	Pro	Val	Ser	Gly	Gly	Val	Asn				
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ttg	ttc	gcc	aac	gac	ggc	agc	ttc	ctg	gag	ctg	ttc	aag	cgg	aag	atg				243
Leu	Phe	Ala	Asn	Asp	Gly	Ser	Phe	Leu	Glu	Leu	Phe	Lys	Arg	Lys	Met				
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Glu	Glu	Glu	Gln	Arg	Gln	Arg	Gln	Glu	Glu	Pro	Pro	Pro	Gly	Pro	Gln				
	75					80					85								
cga	ccc	gac	cag	tcg	gcc	gcc	gcc	gct	ggc	ccc	ggg	gat	ccg	aag	agg				339
Arg	Pro	Asp	Gln	Ser	Ala	Ala	Ala	Ala	Gly	Pro	Gly	Asp	Pro	Lys	Arg				
90					95					100					105				
aag	ggc	ggt	ccg	ggc	tcc	aca	ctt	agc	ttc	gtg	ggc	aaa	cgc	aga	ggc				387
Lys	Gly	Gly	Pro	Gly	Ser	Thr	Leu	Ser	Phe	Val	Gly	Lys	Arg	Arg	Gly				
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ggg	aac	aaa	cta	gcc	ctc	aag	acg	gga	ata	gta	gcc	aag	aag	cag	aag				435
Gly	Asn	Lys	Leu	Ala	Leu	Lys	Thr	Gly	Ile	Val	Ala	Lys	Lys	Gln	Lys				
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acg	gag	gat	gag	gta	tta	aca	agt	aaa	ggt	gac	gcg	tgg	gcc	aag	tac				483
Thr	Glu	Asp	Glu	Val	Leu	Thr	Ser	Lys	Gly	Asp	Ala	Trp	Ala	Lys	Tyr				
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Met	Ala	Glu	Val	Lys	Lys	Tyr	Lys	Ala	His	Gln	Cys	Gly	Asp	Asp	Asp				
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Lys	Thr	Arg	Pro	Leu	Val	Lys													
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 Ser Gly Thr Ser Pro Glu Ser Gly Asp Glu Glu Val Ser Gly Ala Gly  
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 Ser Ser Pro Val Ser Gly Gly Val Asn Leu Phe Ala Asn Asp Gly Ser  
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 Phe Leu Glu Leu Phe Lys Arg Lys Met Glu Glu Glu Gln Arg Gln Arg  
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 Gln Glu Glu Pro Pro Pro Gly Pro Gln Arg Pro Asp Gln Ser Ala Ala  
                   85                  90                  95  
 Ala Ala Gly Pro Gly Asp Pro Lys Arg Lys Gly Gly Pro Gly Ser Thr  
           100                  105                  110  
 Leu Ser Phe Val Gly Lys Arg Arg Gly Gly Asn Lys Leu Ala Leu Lys  
       115                  120                  125  
 Thr Gly Ile Val Ala Lys Lys Gln Lys Thr Glu Asp Glu Val Leu Thr  
   130                  135                  140  
 Ser Lys Gly Asp Ala Trp Ala Lys Tyr Met Ala Glu Val Lys Lys Tyr  
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 Lys Ala His Gln Cys Gly Asp Asp Asp Lys Thr Arg Pro Leu Val Lys  
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 cttcacagca cagttcctgg gaaggtggag ccaccagcct ctccttgaat aactgggaga 180

102260" 88906860

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Met Thr Asp Thr Glu Asn  
1 5

cac gac tca gcc ccc tcc agc acc tct acc tgt tgc ccg ccg atc aca 281  
His Asp Ser Ala Pro Ser Ser Thr Ser Thr Cys Cys Pro Pro Ile Thr  
10 15 20

gcc gga atg cag ctg aaa gat tcc ctg ggg cct ggt tcc aac cgc cca 329  
Ala Gly Met Gln Leu Lys Asp Ser Leu Gly Pro Gly Ser Asn Arg Pro  
25 30 35

ctg tgg act ctg agg cct ctg cat ttg tgg gtg gtc tgc ctg tga 374  
Leu Trp Thr Leu Arg Pro Leu His Leu Trp Val Val Cys Leu  
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ttaatccctt gtccttcatt aaaagcaaaa ctaaag 470

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Val Val Cys Leu  
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Met Lys Leu Lys Asp Thr Lys Ser Arg Pro Lys Gln Ser  
1 5 10

agc tgt ggc aaa ttt cag aca aag gga atc aaa gtt gtg gga aaa tgg 159



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Lys	Glu	Val	Lys	Ile	Asp	Pro	Asn	Met	Phe	Ala	Asp	Gly	Gln	Met	Asp	
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Ala	Gln	Ala	Val	Ser	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Gly	Lys	Ser	Ser	
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Ser	Pro	Lys	Lys	Lys	Ile	Lys	Leu	Lys	Lys	Ser	Lys	Asn	Val	Ala	Thr	
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Glu	Gly	Thr	Ser	Thr	Gln	Lys	Glu	Phe	Glu	Val	Lys	Asp	Pro	Glu	Leu	
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Glu	Ala	Gln	Gly	Asp	Asp	Met	Val	Cys	Asp	Asp	Pro	Glu	Ala	Gly	Glu	
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Met	Thr	Ser	Glu	Asn	Leu	Val	Gln	Thr	Ala	Pro	Lys	Lys	Lys	Lys	Asn	
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Lys	Gly	Lys	Lys	Gly	Leu	Glu	Pro	Ser	Gln	Ser	Thr	Ala	Ala	Lys	Val	
		160					165					170				
ccc	aaa	aaa	gcg	aag	aca	tgg	att	cct	gaa	gtt	cat	gat	cag	aaa	gca	639
Pro	Lys	Lys	Ala	Lys	Thr	Trp	Ile	Pro	Glu	Val	His	Asp	Gln	Lys	Ala	
	175					180					185					
gat	gtg	tca	gct	tgg	aag	gac	ctg	ttt	gtt	ccc	agg	ccg	gtt	ctc	cga	687
Asp	Val	Ser	Ala	Trp	Lys	Asp	Leu	Phe	Val	Pro	Arg	Pro	Val	Leu	Arg	
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Ala	Leu	Ser	Phe	Leu	Gly	Phe	Ser	Ala	Pro	Thr	Pro	Ile	Gln	Ala	Leu	
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Thr	Leu	Ala	Pro	Ala	Ile	Arg	Asp	Lys	Leu	Asp	Ile	Leu	Gly	Ala	Ala	
			225					230					235			
gag	aca	gga	agt	ggg	aaa	act	ctt	gcc	ttt	gcc	atc	cca	atg	att	cat	831
Glu	Thr	Gly	Ser	Gly	Lys	Thr	Leu	Ala	Phe	Ala	Ile	Pro	Met	Ile	His	

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acc gaa gca cca cct gga gag acc aga act gag gcc gga gct gag act Thr Glu Ala Pro Pro Gly Glu Thr Arg Thr Glu Ala Gly Ala Glu Thr 270 275 280 285			927
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gtt ccc aaa cag aat gag aat gag gag gaa aat ctt gat aaa gag cag Val Pro Lys Gln Asn Glu Asn Glu Glu Glu Asn Leu Asp Lys Glu Gln 350 355 360 365			1167
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gca tat cca aag cgt cct ctg ctt gga ctg gtt ctg act ccc act cga Ala Tyr Pro Lys Arg Pro Leu Leu Gly Leu Val Leu Thr Pro Thr Arg 385 390 395			1263
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Glu Lys Gly His Phe Ala Glu Leu Ser Gln Leu Leu Glu Met Leu Asn	
480 485 490	
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Asp Ser Gln Tyr Asn Pro Lys Arg Gln Thr Leu Val Phe Ser Ala Thr	
495 500 505	
ctc acc ctg gtg cat cag gct cct gct cga atc ctt cat aag aag cac	1647
Leu Thr Leu Val His Gln Ala Pro Ala Arg Ile Leu His Lys Lys His	
510 515 520 525	
acc aag aaa atg gat aaa aca gcc aaa ctt gac ctc ctt atg cag aaa	1695
Thr Lys Lys Met Asp Lys Thr Ala Lys Leu Asp Leu Leu Met Gln Lys	
530 535 540	
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Ile Gly Met Arg Gly Lys Pro Lys Val Ile Asp Leu Thr Arg Asn Glu	
545 550 555	
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Ala Thr Val Glu Thr Leu Thr Glu Thr Lys Ile His Cys Glu Thr Asp	
560 565 570	
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Glu Lys Asp Phe Tyr Leu Tyr Tyr Phe Leu Met Gln Tyr Pro Gly Arg	
575 580 585	
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Leu Leu Lys Val Leu Asp Ile Met Pro Leu Thr Leu His Ala Cys Met	
610 615 620	
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625 630 635	
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Asp Cys Val Leu Leu Ala Thr Asp Val Ala Ala Arg Gly Leu Asp Ile	
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Pro Lys Val Gln His Val Ile His Tyr Gln Val Pro Arg Thr Ser Glu	
655 660 665	
att tat gtc cac cga agt ggt cga act gct cga gct acc aat gaa ggc	2127
Ile Tyr Val His Arg Ser Gly Arg Thr Ala Arg Ala Thr Asn Glu Gly	
670 675 680 685	
ctc agt ctg atg ctc att ggg cct gag gat gtg atc aac ttt aag aag	2175
Leu Ser Leu Met Leu Ile Gly Pro Glu Asp Val Ile Asn Phe Lys Lys	
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Gln Thr Lys Tyr Met Asp Val Val Lys Glu Arg Ile Arg Leu Ala Arg  
720 725 730

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735 740 745

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770 775 780

caa aag cag atg aag gtt ctg aag aag gag ctg cgc cac ctg ctg tcc 2463  
Gln Lys Gln Met Lys Val Leu Lys Lys Glu Leu Arg His Leu Leu Ser  
785 790 795

cag cca ctg ttt acg gag agc cag aaa acc aag tat ccc act cag tct 2511  
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800 805 810

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Gly Lys Pro Pro Leu Leu Val Ser Ala Pro Ser Lys Ser Glu Ser Ala  
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830 835 840 845

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850 855

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<210> 38

<211> 859

<212> PRT

<213> Homo sapiens

<400> 38

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Lys	Ile	Asp	Pro	Asn	Met	Phe	Ala	Asp	Gly	Gln	Met	Asp	Asp	Leu	Val
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Cys	Phe	Glu	Glu	Leu	Thr	Asp	Tyr	Gln	Leu	Val	Ser	Pro	Ala	Lys	Asn
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Lys	Lys	Ile	Lys	Leu	Lys	Lys	Ser	Lys	Asn	Val	Ala	Thr	Glu	Gly	Thr
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Ala	Trp	Lys	Asp	Leu	Phe	Val	Pro	Arg	Pro	Val	Leu	Arg	Ala	Leu	Ser
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Phe	Leu	Gly	Phe	Ser	Ala	Pro	Thr	Pro	Ile	Gln	Ala	Leu	Thr	Leu	Ala
	210					215					220				
Pro	Ala	Ile	Arg	Asp	Lys	Leu	Asp	Ile	Leu	Gly	Ala	Ala	Glu	Thr	Gly
	225			230						235				240	
Ser	Gly	Lys	Thr	Leu	Ala	Phe	Ala	Ile	Pro	Met	Ile	His	Ala	Val	Leu
				245					250					255	
Gln	Trp	Gln	Lys	Arg	Asn	Ala	Ala	Pro	Pro	Pro	Ser	Asn	Thr	Glu	Ala
			260					265					270		
Pro	Pro	Gly	Glu	Thr	Arg	Thr	Glu	Ala	Gly	Ala	Glu	Thr	Arg	Ser	Pro
		275					280					285			
Gly	Lys	Ala	Glu	Ala	Glu	Ser	Asp	Ala	Leu	Pro	Asp	Asp	Thr	Val	Ile
	290					295					300				
Glu	Ser	Glu	Ala	Leu	Pro	Ser	Asp	Ile	Ala	Ala	Glu	Ala	Arg	Ala	Lys
	305				310				315					320	
Thr	Gly	Gly	Thr	Val	Ser	Asp	Gln	Ala	Leu	Leu	Phe	Gly	Asp	Asp	Asp
				325					330					335	
Ala	Gly	Glu	Gly	Pro	Ser	Ser	Leu	Ile	Arg	Glu	Lys	Pro	Val	Pro	Lys
			340					345					350		
Gln	Asn	Glu	Asn	Glu	Glu	Glu	Asn	Leu	Asp	Lys	Glu	Gln	Thr	Gly	Asn
		355					360					365			
Leu	Lys	Gln	Glu	Leu	Asp	Asp	Lys	Ser	Ala	Thr	Cys	Lys	Ala	Tyr	Pro
	370					375					380				
Lys	Arg	Pro	Leu	Leu	Gly	Leu	Val	Leu	Thr	Pro	Thr	Arg	Glu	Leu	Ala
	385				390				395					400	
Val	Gln	Val	Lys	Gln	His	Ile	Asp	Ala	Val	Ala	Arg	Phe	Thr	Gly	Ile
				405					410					415	
Lys	Thr	Ala	Ile	Leu	Val	Gly	Gly	Met	Ser	Thr	Gln	Lys	Gln	Gln	Arg
			420					425					430		
Met	Leu	Asn	Arg	Arg	Pro	Glu	Ile	Val	Val	Ala	Thr	Pro	Gly	Arg	Leu
		435					440					445			
Trp	Glu	Leu	Ile	Lys	Glu	Lys	His	Tyr	His	Leu	Arg	Asn	Leu	Arg	Gln
	450					455					460				

Leu Arg Cys Leu Val Val Asp Glu Ala Asp Arg Met Val Glu Lys Gly  
 465 470 475 480  
 His Phe Ala Glu Leu Ser Gln Leu Leu Glu Met Leu Asn Asp Ser Gln  
 485 490 495  
 Tyr Asn Pro Lys Arg Gln Thr Leu Val Phe Ser Ala Thr Leu Thr Leu  
 500 505 510  
 Val His Gln Ala Pro Ala Arg Ile Leu His Lys Lys His Thr Lys Lys  
 515 520 525  
 Met Asp Lys Thr Ala Lys Leu Asp Leu Leu Met Gln Lys Ile Gly Met  
 530 535 540  
 Arg Gly Lys Pro Lys Val Ile Asp Leu Thr Arg Asn Glu Ala Thr Val  
 545 550 555 560  
 Glu Thr Leu Thr Glu Thr Lys Ile His Cys Glu Thr Asp Glu Lys Asp  
 565 570 575  
 Phe Tyr Leu Tyr Tyr Phe Leu Met Gln Tyr Pro Gly Arg Ser Leu Val  
 580 585 590  
 Phe Ala Asn Ser Ile Ser Cys Ile Lys Arg Leu Ser Gly Leu Leu Lys  
 595 600 605  
 Val Leu Asp Ile Met Pro Leu Thr Leu His Ala Cys Met His Gln Lys  
 610 615 620  
 Gln Arg Leu Arg Asn Leu Glu Gln Phe Ala Arg Leu Glu Asp Cys Val  
 625 630 635 640  
 Leu Leu Ala Thr Asp Val Ala Ala Arg Gly Leu Asp Ile Pro Lys Val  
 645 650 655  
 Gln His Val Ile His Tyr Gln Val Pro Arg Thr Ser Glu Ile Tyr Val  
 660 665 670  
 His Arg Ser Gly Arg Thr Ala Arg Ala Thr Asn Glu Gly Leu Ser Leu  
 675 680 685  
 Met Leu Ile Gly Pro Glu Asp Val Ile Asn Phe Lys Lys Ile Tyr Lys  
 690 695 700  
 Thr Leu Lys Lys Asp Glu Asp Ile Pro Leu Phe Pro Val Gln Thr Lys  
 705 710 715 720  
 Tyr Met Asp Val Val Lys Glu Arg Ile Arg Leu Ala Arg Gln Ile Glu  
 725 730 735  
 Lys Ser Glu Tyr Arg Asn Phe Gln Ala Cys Leu His Asn Ser Trp Ile  
 740 745 750  
 Glu Gln Ala Ala Ala Leu Glu Ile Glu Leu Glu Glu Asp Met Tyr  
 755 760 765  
 Lys Gly Gly Lys Ala Asp Gln Gln Glu Glu Arg Arg Arg Gln Lys Gln  
 770 775 780  
 Met Lys Val Leu Lys Lys Glu Leu Arg His Leu Leu Ser Gln Pro Leu  
 785 790 795 800  
 Phe Thr Glu Ser Gln Lys Thr Lys Tyr Pro Thr Gln Ser Gly Lys Pro  
 805 810 815  
 Pro Leu Leu Val Ser Ala Pro Ser Lys Ser Glu Ser Ala Leu Ser Cys  
 820 825 830  
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<210> 39  
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 <212> DNA  
 <213> Homo sapiens

<220>

<221> CDS

<222> (15)..(998)

<400> 39

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		1				5					10					
tgc	ggc	cgt	ggg	tgg	tcg	cgg	gcg	atg	cgg	ggc	tgc	cag	ctc	ctc	ggg	98
Cys	Gly	Arg	Gly	Trp	Ser	Arg	Ala	Met	Arg	Gly	Cys	Gln	Leu	Leu	Gly	
		15					20					25				
ctt	cgt	agc	tct	tgg	ccc	ggg	gac	cta	cta	agt	gct	cgg	ctc	ttg	tcc	146
Leu	Arg	Ser	Ser	Trp	Pro	Gly	Asp	Leu	Leu	Ser	Ala	Arg	Leu	Leu	Ser	
		30				35					40					
caa	gag	aag	cgg	gca	gcg	gaa	acg	cac	ttt	ggg	ttt	gag	act	gtg	tcg	194
Gln	Glu	Lys	Arg	Ala	Ala	Glu	Thr	His	Phe	Gly	Phe	Glu	Thr	Val	Ser	
		45			50					55					60	
gaa	gag	gag	aag	ggg	ggc	aaa	gtc	tat	cag	gtg	ttt	gaa	agt	gtg	gct	242
Glu	Glu	Glu	Lys	Gly	Gly	Lys	Val	Tyr	Gln	Val	Phe	Glu	Ser	Val	Ala	
				65					70					75		
aag	aag	tat	gat	gtg	atg	aat	gat	atg	atg	agt	ctt	ggt	atc	cat	cgt	290
Lys	Lys	Tyr	Asp	Val	Met	Asn	Asp	Met	Met	Ser	Leu	Gly	Ile	His	Arg	
			80					85					90			
gtt	tgg	aag	gat	ttg	ctg	ctc	tgg	aag	atg	cac	ccg	ctt	cct	ggg	acc	338
Val	Trp	Lys	Asp	Leu	Leu	Leu	Trp	Lys	Met	His	Pro	Leu	Pro	Gly	Thr	
		95					100					105				
cag	ctg	ctt	gat	gtt	gct	gga	ggc	aca	ggt	gac	att	gca	ttc	cgg	ttc	386
Gln	Leu	Leu	Asp	Val	Ala	Gly	Gly	Thr	Gly	Asp	Ile	Ala	Phe	Arg	Phe	
	110					115					120					
ctt	aat	tat	gtt	cag	tcc	cag	cat	cag	aga	aaa	cag	aag	agg	cag	tta	434
Leu	Asn	Tyr	Val	Gln	Ser	Gln	His	Gln	Arg	Lys	Gln	Lys	Arg	Gln	Leu	
	125				130					135					140	
agg	gcc	caa	caa	aat	tta	tcc	tgg	gaa	gaa	att	gcc	aaa	gag	tac	cag	482
Arg	Ala	Gln	Gln	Asn	Leu	Ser	Trp	Glu	Glu	Ile	Ala	Lys	Glu	Tyr	Gln	
				145					150					155		
aat	gaa	gaa	gat	tcc	ttg	ggc	ggg	tct	cgt	gtc	gtg	gtg	tgt	gac	atc	530
Asn	Glu	Glu	Asp	Ser	Leu	Gly	Gly	Ser	Arg	Val	Val	Val	Cys	Asp	Ile	
			160				165						170			
aac	aag	gag	atg	cta	aag	gtt	gga	aag	cag	aaa	gcc	ttg	gct	caa	gga	578
Asn	Lys	Glu	Met	Leu	Lys	Val	Gly	Lys	Gln	Lys	Ala	Leu	Ala	Gln	Gly	
		175					180					185				
tac	aga	gct	gga	ctt	gca	tgg	gta	tta	gga	gat	gct	gaa	gaa	ctg	ccc	626
Tyr	Arg	Ala	Gly	Leu	Ala	Trp	Val	Leu	Gly	Asp	Ala	Glu	Glu	Leu	Pro	
		190				195					200					

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ttt gat gat gac aag ttt gat att tac acc att gcc ttt ggg atc cgg	674
Phe Asp Asp Asp Lys Phe Asp Ile Tyr Thr Ile Ala Phe Gly Ile Arg	
205 210 215 220	
aat gtc aca cac att gat cag gca ctc cag gaa gct cat cgg gtg ctg	722
Asn Val Thr His Ile Asp Gln Ala Leu Gln Glu Ala His Arg Val Leu	
225 230 235	
aaa cca gga gga cgg ttt ctc tgt ctg gaa ttt agc caa gtg aac aat	770
Lys Pro Gly Gly Arg Phe Leu Cys Leu Glu Phe Ser Gln Val Asn Asn	
240 245 250	
ccc ctc ata tcc agg ctt tat gat cta tat agc ttc cag gtc atc cct	818
Pro Leu Ile Ser Arg Leu Tyr Asp Leu Tyr Ser Phe Gln Val Ile Pro	
255 260 265	
gtc ctg gga gag gtc atc gct gga gac tgg aag tcc tat cag tac ctt	866
Val Leu Gly Glu Val Ile Ala Gly Asp Trp Lys Ser Tyr Gln Tyr Leu	
270 275 280	
gta gag agt atc cga agg ttt ccg tct cag gaa gag ttc aag gac atg	914
Val Glu Ser Ile Arg Arg Phe Pro Ser Gln Glu Glu Phe Lys Asp Met	
285 290 295 300	
ata gaa gat gca ggc ttt cac aag gtg act tac gaa agt cta aca tca	962
Ile Glu Asp Ala Gly Phe His Lys Val Thr Tyr Glu Ser Leu Thr Ser	
305 310 315	
ggc att gtg gcc att cat tct ggc ttc aaa ctt taa ttcctttcct	1008
Gly Ile Val Ala Ile His Ser Gly Phe Lys Leu	
320 325	
atcatggagc atgaaccagt catatcctgt tgaaagcctg gaactgaagg ataatctggc	1068
aatgagaca gcagcagagc atctcctctt aaggatacgt gccttggaact catgtttgaa	1128
tcgaacagtc tcaaagtgga agaacaaatt cttgtcactt ttttacagct ttctttggag	1188
ctgcttcagt ccatctccca gaggcatttg gtctgtatct ttgctcaact gctaatttct	1248
cttggtctgta ggggtgtgtgg ttaaggtaca accacccta aagctcagtt ttgaagtgag	1308
tgtatttata gcttctctgc tgggtgtgcc ttctagaggg atgatagatc atttgaacct	1368
aatgacaatt tttaaccaga aaatttaatt gtacctgaat caacctttca gcctaggacg	1428
aagtctaggc ccaagtcaga gtattaatga tcatgagaat tgtgtgctga accagtaaac	1488
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<210> 40

<211> 327

<212> PRT

<213> Homo sapiens

<400> 40



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 20 25 30  
 Trp Pro Gly Asp Leu Leu Ser Ala Arg Leu Leu Ser Gln Glu Lys Arg  
 35 40 45  
 Ala Ala Glu Thr His Phe Gly Phe Glu Thr Val Ser Glu Glu Glu Lys  
 50 55 60  
 Gly Gly Lys Val Tyr Gln Val Phe Glu Ser Val Ala Lys Lys Tyr Asp  
 65 70 75 80  
 Val Met Asn Asp Met Met Ser Leu Gly Ile His Arg Val Trp Lys Asp  
 85 90 95  
 Leu Leu Leu Trp Lys Met His Pro Leu Pro Gly Thr Gln Leu Leu Asp  
 100 105 110  
 Val Ala Gly Gly Thr Gly Asp Ile Ala Phe Arg Phe Leu Asn Tyr Val  
 115 120 125  
 Gln Ser Gln His Gln Arg Lys Gln Lys Arg Gln Leu Arg Ala Gln Gln  
 130 135 140  
 Asn Leu Ser Trp Glu Glu Ile Ala Lys Glu Tyr Gln Asn Glu Glu Asp  
 145 150 155 160  
 Ser Leu Gly Gly Ser Arg Val Val Val Cys Asp Ile Asn Lys Glu Met  
 165 170 175  
 Leu Lys Val Gly Lys Gln Lys Ala Leu Ala Gln Gly Tyr Arg Ala Gly  
 180 185 190  
 Leu Ala Trp Val Leu Gly Asp Ala Glu Glu Leu Pro Phe Asp Asp Asp  
 195 200 205  
 Lys Phe Asp Ile Tyr Thr Ile Ala Phe Gly Ile Arg Asn Val Thr His  
 210 215 220  
 Ile Asp Gln Ala Leu Gln Glu Ala His Arg Val Leu Lys Pro Gly Gly  
 225 230 235 240  
 Arg Phe Leu Cys Leu Glu Phe Ser Gln Val Asn Asn Pro Leu Ile Ser  
 245 250 255  
 Arg Leu Tyr Asp Leu Tyr Ser Phe Gln Val Ile Pro Val Leu Gly Glu  
 260 265 270  
 Val Ile Ala Gly Asp Trp Lys Ser Tyr Gln Tyr Leu Val Glu Ser Ile  
 275 280 285  
 Arg Arg Phe Pro Ser Gln Glu Glu Phe Lys Asp Met Ile Glu Asp Ala  
 290 295 300  
 Gly Phe His Lys Val Thr Tyr Glu Ser Leu Thr Ser Gly Ile Val Ala  
 305 310 315 320  
 Ile His Ser Gly Phe Lys Leu  
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<210> 41  
 <211> 737  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (127)..(387)

<400> 41  
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 aaaacgctag agcggcgagt tggttacctgc gtcctctgac ctgagagcga aggggaaagc 120

09390688.092701

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ggcgag atg act gac cgc tac acc atc cat agc cag ctg gag cac ctg      168
  Met Thr Asp Arg Tyr Thr Ile His Ser Gln Leu Glu His Leu
    1             5             10

cag tcc aag tac atc ggc acg ggc cac gcc gac acc acc aag tgg gag      216
Gln Ser Lys Tyr Ile Gly Thr Gly His Ala Asp Thr Thr Lys Trp Glu
  15             20             25             30

tgg ctg gtg aac caa cac cgc gac tcg tac tgc tcc tac atg ggc cac      264
Trp Leu Val Asn Gln His Arg Asp Ser Tyr Cys Ser Tyr Met Gly His
           35             40             45

ttc gac ctt ctc aac tac ttc gcc att gcg gag aat gag agc aaa gcg      312
Phe Asp Leu Leu Asn Tyr Phe Ala Ile Ala Glu Asn Glu Ser Lys Ala
           50             55             60

cga gtc cgc ttc aac ttg atg gaa aag atg ctt cag cct tgt gga ccg      360
Arg Val Arg Phe Asn Leu Met Glu Lys Met Leu Gln Pro Cys Gly Pro
           65             70             75

cca gcc gac aag ccc gag gag aac tga gactctgcct taccacctca      407
Pro Ala Asp Lys Pro Glu Glu Asn
   80             85

gtgcgggggca cctctcccag cgtttctccg gtttgccaat cctcttaagt attcctgtct 467

ccaaaggacc ggctctccat ggctcctgcg cctcgtgctt tccgcgtaca gaagtgcttg 527

cccggggagt cccgcctgac ctgccttcat gtggaccctt agaacagcac tgggagacca 587

gcaggactcc tgagaactgt gctggtggag aggtcctaga gccggcgagc gtttgagaag 647

agggcatggc gctggagtga gatgggattt ggcgtctcgt ttttggctaa ttgattgtca 707

ttggcttttt ccataaagtt tagaaatcgt      737

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<210> 42  
 <211> 86  
 <212> PRT  
 <213> Homo sapiens

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<400> 42
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Lys Tyr Ile Gly Thr Gly His Ala Asp Thr Thr Lys Trp Glu Trp Leu
           20             25             30
Val Asn Gln His Arg Asp Ser Tyr Cys Ser Tyr Met Gly His Phe Asp
           35             40             45
Leu Leu Asn Tyr Phe Ala Ile Ala Glu Asn Glu Ser Lys Ala Arg Val
           50             55             60
Arg Phe Asn Leu Met Glu Lys Met Leu Gln Pro Cys Gly Pro Pro Ala
           65             70             75             80
Asp Lys Pro Glu Glu Asn
           85

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**SECRET**

<400> 43

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Met Ser Thr Pro Pro Leu Ala Ala Ser  
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cgg gaa gtc aac acg gcg tcg ctg tgc cgc atc ggg cag gag aca gtg 207  
Arg Glu Val Asn Thr Ala Ser Leu Cys Arg Ile Gly Gln Glu Thr Val  
30 35 40

atg cag ctg cca aat ggt gtc act tac cac act gga aca tat caa gac 303  
Met Gln Leu Pro Asn Gly Val Thr Tyr His Thr Gly Thr Tyr Gln Asp  
60 65 70

cgg tta aca aag cta cag gat aat ctt cgc caa ctt tca gtt ctc ttc 351  
 Arg Leu Thr Lys Leu Gln Asp Asn Leu Arg Gln Leu Ser Val Leu Phe  
 75 80 85

agg aag ctg aga ttg gta tat gac aaa tgc aat gaa aac tgt ggt ggg 399  
Arg Lys Leu Arg Leu Val Tyr Asp Lys Cys Asn Glu Asn Cys Gly Gly  
90 95 100 105

atg gat ccc att cca gtc gag caa ctt att cca tat gtg gaa gaa gat 447  
Met Asp Pro Ile Pro Val Glu Gln Leu Ile Pro Tyr Val Glu Glu Asp  
110 115 120

ggc tca aag aat gat gat cgg gct ggc cca cct cgt ttt gct agt gaa 495  
Gly Ser Lys Asn Asp Asp Arg Ala Gly Pro Pro Arg Phe Ala Ser Glu  
125 130 135

gag agg cga gaa att gct gaa gta aat aaa aaa ctc aaa cag aag aat 543  
Glu Arg Arg Glu Ile Ala Glu Val Asn Lys Lys Leu Lys Gln Lys Asn  
140 145 150

caa cag ctg aaa caa att atg gat caa tta cga aat ctc atc tgg gat 591  
Gln Gln Leu Lys Gln Ile Met Asp Gln Leu Arg Asn Leu Ile Trp Asp  
155 160 165

ata aat gcc atg ttg gca atg agg aac taa gctgatattt aaatttcctg 641  
 Ile Asn Ala Met Leu Ala Met Arg Asn  
 170 175

ctttacacat gttataccat tgttttttcc ctcaagtatt ttttccctgt gaagaagatt 701  
 atttatctgc ttttatttta gtcactaaaa cttaaagtttt tattttttaca ttgtgatttt 761  
 tacattaaaa tattaacttt ttttaattgct attttatgaa agattattgt aataaacttt 821  
 gatgggggttt gtatttttggg taatcttcat gaattgaata attgtttttt taaagcaaaa 881  
 taaagttttt taaataaatg tt 903

<210> 44  
 <211> 178  
 <212> PRT  
 <213> Homo sapiens

<400> 44  
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 Ala Gly Pro Gln Ala Gln Gln Ala Ala Arg Glu Val Asn Thr Ala Ser  
 20 25 30  
 Leu Cys Arg Ile Gly Gln Glu Thr Val Gln Asp Ile Val Tyr Arg Thr  
 35 40 45  
 Met Glu Ile Phe Gln Leu Leu Arg Asn Met Gln Leu Pro Asn Gly Val  
 50 55 60  
 Thr Tyr His Thr Gly Thr Tyr Gln Asp Arg Leu Thr Lys Leu Gln Asp  
 65 70 75 80  
 Asn Leu Arg Gln Leu Ser Val Leu Phe Arg Lys Leu Arg Leu Val Tyr  
 85 90 95  
 Asp Lys Cys Asn Glu Asn Cys Gly Gly Met Asp Pro Ile Pro Val Glu  
 100 105 110  
 Gln Leu Ile Pro Tyr Val Glu Glu Asp Gly Ser Lys Asn Asp Asp Arg  
 115 120 125  
 Ala Gly Pro Pro Arg Phe Ala Ser Glu Glu Arg Arg Glu Ile Ala Glu  
 130 135 140  
 Val Asn Lys Lys Leu Lys Gln Lys Asn Gln Gln Leu Lys Gln Ile Met  
 145 150 155 160  
 Asp Gln Leu Arg Asn Leu Ile Trp Asp Ile Asn Ala Met Leu Ala Met  
 165 170 175  
 Arg Asn

<210> 45  
 <211> 1170  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (187)..(540)

<400> 45  
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ccaagatcct ttcaggatat ttggtttttt gggcgcgaca caaatcgagg tgagggaaga 120

gagaggaaaa tccctgaat ccctgcagga ttaatttatt caaaaaggaa ataaaaaata 180

ctcaat atg caa aag tct tgt gaa gaa aat gag gga aaa cca cag aac 228  
Met Gln Lys Ser Cys Glu Glu Asn Glu Gly Lys Pro Gln Asn  
1 5 10

atg cca aag gcc gag gaa gat cgc cct ttg gag gat gta cca cag gag 276  
Met Pro Lys Ala Glu Glu Asp Arg Pro Leu Glu Asp Val Pro Gln Glu  
15 20 25 30

gca gaa gga aat cct caa cct tcc gaa gaa ggc gta agc cag gaa gca 324  
Ala Glu Gly Asn Pro Gln Pro Ser Glu Glu Gly Val Ser Gln Glu Ala  
35 40 45

gaa gga aac ccc aga gga ggg ccg aat cag cct ggc cag gga ttt aaa 372  
Glu Gly Asn Pro Arg Gly Gly Pro Asn Gln Pro Gly Gln Gly Phe Lys  
50 55 60

gag gac aca ccc gtt agg cat ttg gac cct gaa gaa atg ata aga gga 420  
Glu Asp Thr Pro Val Arg His Leu Asp Pro Glu Glu Met Ile Arg Gly  
65 70 75

gta gat gag ctt gaa agg ctt agg gaa gag ata aga aga gta aga aac 468  
Val Asp Glu Leu Glu Arg Leu Arg Glu Glu Ile Arg Arg Val Arg Asn  
80 85 90

aag ttt gtg atg atg cat tgg aag caa aga cat tca cgc agc cgt cct 516  
Lys Phe Val Met Met His Trp Lys Gln Arg His Ser Arg Ser Arg Pro  
95 100 105 110

tat cct gtg tgc ttt agg cct tga attcattttt gcctaataatt aaaatctggc 570  
Tyr Pro Val Cys Phe Arg Pro  
115

cccagctttc tttctgttag cattttctga tgtatctttg acctccattt tacttttaat 630

catctgatga aattttgttt taggtaattt ccttggtacc agcatctcat tggattttgg 690

attttgaccc attttccagg tctatttttc aattggaaac tttcacacat ttgcatggga 750

atatgttcat tccatgttgt aaagtaaaac ataacagggt atggcaaagc agcatattta 810

atatcagctc acatatgtag gataaaattc caaactttgt gtgtgtgcgt gtgtgtatac 870

atacatccat ataacatata tcacaaactt aaccaagctt atttctgtgt ggtgtgaaat 930

tttattttgtt ttcttctttt tgttcttttt gcttatatgt acttttttaat gaacacgtgt 990

ctcacacaca aaaagaatta aggatttttt ttacaagtaa gagtcaaata atttgcaacc 1050

agcttatgag ggcaatgggg gcacctaaac tcttgatgaa agaactttta aaagaaatgt 1110

aaacctcaaa ttacctctgg atctcttagc cagaggaata aactggcaat tattacagat 1170

<210> 46  
 <211> 117  
 <212> PRT  
 <213> Homo sapiens

<400> 46  
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 20 25 30  
 Gly Asn Pro Gln Pro Ser Glu Glu Gly Val Ser Gln Glu Ala Glu Gly  
 35 40 45  
 Asn Pro Arg Gly Gly Pro Asn Gln Pro Gly Gln Gly Phe Lys Glu Asp  
 50 55 60  
 Thr Pro Val Arg His Leu Asp Pro Glu Glu Met Ile Arg Gly Val Asp  
 65 70 75 80  
 Glu Leu Glu Arg Leu Arg Glu Glu Ile Arg Arg Val Arg Asn Lys Phe  
 85 90 95  
 Val Met Met His Trp Lys Gln Arg His Ser Arg Ser Arg Pro Tyr Pro  
 100 105 110  
 Val Cys Phe Arg Pro  
 115

<210> 47  
 <211> 404  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (105)..(365)

<400> 47  
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 Met Glu Leu Ser  
 1  
 gcc gaa tac ctc cgc gag aag ctg cag cgg gac ctg gag gcg gag cat 164  
 Ala Glu Tyr Leu Arg Glu Lys Leu Gln Arg Asp Leu Glu Ala Glu His  
 5 10 15 20  
 gtg gag gtg gag gac acg acc ctc aac cgt tgc tcc tgt agc ttc cga 212  
 Val Glu Val Glu Asp Thr Thr Leu Asn Arg Cys Ser Cys Ser Phe Arg  
 25 30 35  
 gtc ctg gtg gtg tcg gcc aag ttc gag ggg aaa ccg ctg ctt cag aga 260  
 Val Leu Val Val Ser Ala Lys Phe Glu Gly Lys Pro Leu Leu Gln Arg  
 40 45 50  
 cac agg ctg gtg aac gcg tgc cta gca gaa gag ctc ccg cac atc cat 308  
 His Arg Leu Val Asn Ala Cys Leu Ala Glu Glu Leu Pro His Ile His  
 55 60 65

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Ala Phe Glu Gln Lys Thr Leu Thr Pro Asp Gln Trp Ala Arg Glu Arg  
70 75 80

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Gln Lys  
85

<210> 48  
<211> 86  
<212> PRT  
<213> Homo sapiens

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Glu Ala Glu His Val Glu Val Glu Asp Thr Thr Leu Asn Arg Cys Ser  
20 25 30  
Cys Ser Phe Arg Val Leu Val Val Ser Ala Lys Phe Glu Gly Lys Pro  
35 40 45  
Leu Leu Gln Arg His Arg Leu Val Asn Ala Cys Leu Ala Glu Glu Leu  
50 55 60  
Pro His Ile His Ala Phe Glu Gln Lys Thr Leu Thr Pro Asp Gln Trp  
65 70 75 80  
Ala Arg Glu Arg Gln Lys  
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<211> 752  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (95)..(634)

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Met Ala Ala Thr Glu Pro Ile  
1 5

ttg gcg gcc act ggg agt ccc gcg gcg gtg cca ccg gag aaa ctg gaa 163  
Leu Ala Ala Thr Gly Ser Pro Ala Ala Val Pro Pro Glu Lys Leu Glu  
10 15 20

gga gcc ggt tcg agc tca gcc cct gag cgt aac tgt gtg ggc tcc tcg 211  
Gly Ala Gly Ser Ser Ser Ala Pro Glu Arg Asn Cys Val Gly Ser Ser  
25 30 35

ctg cca gag gcc tca ccg cct gcc cct gag cct tcc agt ccc aac gcc 259  
Leu Pro Glu Ala Ser Pro Pro Ala Pro Glu Pro Ser Ser Pro Asn Ala  
40 45 50 55

gcg gtc cct gaa gcc atc cct acg ccc cga gct gcg gcc tcc gcg gcc 307  
Ala Val Pro Glu Ala Ile Pro Thr Pro Arg Ala Ala Ala Ser Ala Ala  
60 65 70

ctg gag ctg cct ctc ggg ccc gca ccc gtg agc gta gcg cct cag gcc 355  
Leu Glu Leu Pro Leu Gly Pro Ala Pro Val Ser Val Ala Pro Gln Ala  
75 80 85

gaa gct gaa gcg cgc tcc aca cca ggc ccc gcc ggc tct aga ctc ggt 403  
Glu Ala Glu Ala Arg Ser Thr Pro Gly Pro Ala Gly Ser Arg Leu Gly  
90 95 100

ccc gag acg ttc cgc cag cgt ttc cgg cag ttc cgc tac cag gat gcg 451  
Pro Glu Thr Phe Arg Gln Arg Phe Arg Gln Phe Arg Tyr Gln Asp Ala  
105 110 115

gcg ggt ccc cgg gag gct ttc cgg cag ctg cgg gag ctg tcc cgc cag 499  
Ala Gly Pro Arg Glu Ala Phe Arg Gln Leu Arg Glu Leu Ser Arg Gln  
120 125 130 135

tgg ctg cgg cct gac atc cgc acc aag gag cag atc gtg gag atg ctg 547  
Trp Leu Arg Pro Asp Ile Arg Thr Lys Glu Gln Ile Val Glu Met Leu  
140 145 150

gtg caa gag cag ctg ctc gcc atc ctg ccc gag gcg gct cgg gcc cgg 595  
Val Gln Glu Gln Leu Leu Ala Ile Leu Pro Glu Ala Ala Arg Ala Arg  
155 160 165

cgg atc cgc cgc cgc acg gat gtg cgc atc act ggc tga gcggtggagc 644  
Arg Ile Arg Arg Arg Thr Asp Val Arg Ile Thr Gly  
170 175

tgcgggcggc cagggccggg cgctctgtgc ggactggggc catgatcggg cccggggggcc 704

tgagcctggg accccacccc gtgttaatga aaaatgagtt ttggcagc 752

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<211> 179  
<212> PRT  
<213> Homo sapiens

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Arg Asn Cys Val Gly Ser Ser Leu Pro Glu Ala Ser Pro Pro Ala Pro  
35 40 45  
Glu Pro Ser Ser Pro Asn Ala Ala Val Pro Glu Ala Ile Pro Thr Pro  
50 55 60  
Arg Ala Ala Ala Ser Ala Ala Leu Glu Leu Pro Leu Gly Pro Ala Pro  
65 70 75 80  
Val Ser Val Ala Pro Gln Ala Glu Ala Glu Arg Ser Thr Pro Gly  
85 90 95  
Pro Ala Gly Ser Arg Leu Gly Pro Glu Thr Phe Arg Gln Arg Phe Arg  
100 105 110



Gln Phe Arg Tyr Gln Asp Ala Ala Gly Pro Arg Glu Ala Phe Arg Gln  
 115 120 125  
 Leu Arg Glu Leu Ser Arg Gln Trp Leu Arg Pro Asp Ile Arg Thr Lys  
 130 135 140  
 Glu Gln Ile Val Glu Met Leu Val Gln Glu Gln Leu Leu Ala Ile Leu  
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<210> 51  
 <211> 1222  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (219)..(788)

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 ctgaccgcgt gatccgcccgc cctcggcctc cgaaactgct gaaattacag gcgtgagcca 180  
 ccgcgcccgg cctccctctt tccgtgcgcg ccgtggga atg gaa aca tct gcc cca 236  
 Met Glu Thr Ser Ala Pro  
 1 5  
 cgt gcc gga agc caa gtg gtg gcg aca act gcg cgc cac tcc gcg gcc 284  
 Arg Ala Gly Ser Gln Val Val Ala Thr Thr Ala Arg His Ser Ala Ala  
 10 15 20  
 tac cgc gca gat cct cta cgt gtg tcc tcg cga gac aag ctc acc gaa 332  
 Tyr Arg Ala Asp Pro Leu Arg Val Ser Ser Arg Asp Lys Leu Thr Glu  
 25 30 35  
 atg gcc gcg tcc agt caa gga aac ttt gag gga aat ttt gag tca ctg 380  
 Met Ala Ala Ser Ser Gln Gly Asn Phe Glu Gly Asn Phe Glu Ser Leu  
 40 45 50  
 gac ctt gcg gaa ttt gct aag aag cag cca tgg tgg cgt aag ctg ttc 428  
 Asp Leu Ala Glu Phe Ala Lys Lys Gln Pro Trp Trp Arg Lys Leu Phe  
 55 60 65 70  
 ggg cag gaa tct gga cct tca gca gaa aag tat agc gtg gca acc cag 476  
 Gly Gln Glu Ser Gly Pro Ser Ala Glu Lys Tyr Ser Val Ala Thr Gln  
 75 80 85  
 ctg ttc att gga ggt gtc act gga tgg tgc aca ggt ttc ata ttc cag 524  
 Leu Phe Ile Gly Gly Val Thr Gly Trp Cys Thr Gly Phe Ile Phe Gln  
 90 95 100  
 aag gtt gga aag ttg gct gca aca gct gtg gga ggt gga ttt ttt ctc 572  
 Lys Val Gly Lys Leu Ala Ala Thr Ala Val Gly Gly Gly Phe Phe Leu

105	110	115	
ctt cag ctt gca aac cat act ggg tac atc aaa gtt gac tgg caa cga			620
Leu Gln Leu Ala Asn His Thr Gly Tyr Ile Lys Val Asp Trp Gln Arg			
120	125	130	
gtg gag aag gac atg aag aaa gcc aaa gag cag ctg aag atc cgt aag			668
Val Glu Lys Asp Met Lys Lys Ala Lys Glu Gln Leu Lys Ile Arg Lys			
135	140	145	150
agc aat cag ata cct act gag gtc agg agc aaa gct gag gag gtg gtg			716
Ser Asn Gln Ile Pro Thr Glu Val Arg Ser Lys Ala Glu Glu Val Val			
155	160	165	
tca ttt gtg aag aag aat gtt cta gta act ggg gga ttt ttc gga ggc			764
Ser Phe Val Lys Lys Asn Val Leu Val Thr Gly Gly Phe Phe Gly Gly			
170	175	180	
ttt ctg ctt ggc atg gca tcc taa ggaagatgac ctcatgttca ttgttcctgg			818
Phe Leu Leu Gly Met Ala Ser			
185			
ttttttccag ccagcagcct ctacactcca tcataggaca tcgagtcctt cctcctcttc			878
tcccatgcct tcttccctgc catggcaaat ctgagtggct tctctaagca tctgctggta			938
caagtcaatg tggcaccatg agcttcatgg tggcagaaga gacaatagtc cttagctctc			998
ctcccagtac accccctact tggccagtct gtaggccaac aagaaggttc ctttaccctc			1058
atgcaagaca cttatgagaa cacattacaa gatggctgac cgtggaggat gagtggatcc			1118
tgaaaggttg tcccaaactg ttgatttggg aaagaaataa gcacatagat aaccttattg			1178
tgtgctgcat ggaaaggaac tgaatacatt tgcctttaag catg			1222

<210> 52  
 <211> 189  
 <212> PRT  
 <213> Homo sapiens

<400> 52

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Arg Asp Lys Leu Thr Glu Met Ala Ala Ser Ser Gln Gly Asn Phe Glu	
35 40 45	
Gly Asn Phe Glu Ser Leu Asp Leu Ala Glu Phe Ala Lys Lys Gln Pro	
50 55 60	
Trp Trp Arg Lys Leu Phe Gly Gln Glu Ser Gly Pro Ser Ala Glu Lys	
65 70 75 80	
Tyr Ser Val Ala Thr Gln Leu Phe Ile Gly Gly Val Thr Gly Trp Cys	
85 90 95	
Thr Gly Phe Ile Phe Gln Lys Val Gly Lys Leu Ala Ala Thr Ala Val	
100 105 110	

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Gly Gly Gly Phe Phe Leu Leu Gln Leu Ala Asn His Thr Gly Tyr Ile  
 115 120 125  
 Lys Val Asp Trp Gln Arg Val Glu Lys Asp Met Lys Lys Ala Lys Glu  
 130 135 140  
 Gln Leu Lys Ile Arg Lys Ser Asn Gln Ile Pro Thr Glu Val Arg Ser  
 145 150 155 160  
 Lys Ala Glu Glu Val Val Ser Phe Val Lys Lys Asn Val Leu Val Thr  
 165 170 175  
 Gly Gly Phe Phe Gly Gly Phe Leu Leu Gly Met Ala Ser  
 180 185

<210> 53  
 <211> 1209  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (95)..(448)

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 Met Ile Ser Gly Leu Phe Met  
 1 5  
 tcg ttg tgc tgc gcc ggg agc cac cgc cct ccg gag aca ggg cag ctc 163  
 Ser Leu Cys Cys Ala Gly Ser His Arg Pro Pro Glu Thr Gly Gln Leu  
 10 15 20  
 ccc tac gac cct agc gcc tcc gcc ctc cgc ggc ccc tct cct ctc ttc 211  
 Pro Tyr Asp Pro Ser Ala Ser Ala Leu Arg Gly Pro Ser Pro Leu Phe  
 25 30 35  
 ctg ctc tgt ccc tcc ttc tcc atc agg gag cag cgt gac ttc agc gag 259  
 Leu Leu Cys Pro Ser Phe Ser Ile Arg Glu Gln Arg Asp Phe Ser Glu  
 40 45 50 55  
 tcc cgc gag cac ctg gct aga cag tta aca agc acg tcc ttc cag cct 307  
 Ser Arg Glu His Leu Ala Arg Gln Leu Thr Ser Thr Ser Phe Gln Pro  
 60 65 70  
 gag cca gcg cag gtt tgg gag ggg gct tcc tgg ccc ccc cca cgg tgt 355  
 Glu Pro Ala Gln Val Trp Glu Gly Ala Ser Trp Pro Pro Pro Arg Cys  
 75 80 85  
 tcc agc ccc tcc tct ctt ccg ccc cct agt ctc cca ccc ttc cct ccc 403  
 Ser Ser Pro Ser Ser Leu Pro Pro Pro Ser Leu Pro Pro Phe Pro Pro  
 90 95 100  
 cgt agt gac caa ttc cta tct ctt ccc tct ccg cag gct caa tga 448  
 Arg Ser Asp Gln Phe Leu Ser Leu Pro Ser Pro Gln Ala Gln  
 105 110 115  
 atcgaatgaa tgtgaacttc ttcattctgtg aaaaatcttt tttttttcca ttttgttctg 508

tttgggggct tctgttttgt ttggcgagag agcgatggct gccgtgggga gtactgggga 568  
gccctcgcgg caagcagggg ggggggggact tgggggcatg ccgggccctc actctctcgc 628  
ctgttctgtg tctcacatgc tttttctttc aaaattggga tccttccatg ttgagccagc 688  
cagagaagat agcgagatct aaatctctgc caaaaaaaaa aaaaacttaa aaattaaaaa 748  
cacaaagagc aaagcagaac ttataaaatt atatatatat atattaaaaa gtctctattc 808  
ttcaccccc agccttcctg aacctgcctc tctgaggata aagcaattca ttttctccca 868  
ccctcgcccc tcttggtttt aaaataaaact tttaaaaagg aaaaaaaaaa gtcactcttg 928  
ctatttcttt tttttagtta gaggtggaac attccttgga ccagggtgtg tattgcagga 988  
ccccctccc cagcagccaa gccccctctt ctctccctcc cgccctggct cagctccgc 1048  
ggccccgccc gtccccctc ccaggactgg tctgttgtct tttcatctgt tcaagaggag 1108  
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<210> 54  
<211> 117  
<212> PRT  
<213> Homo sapiens

<400> 54  
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20 25 30  
Arg Gly Pro Ser Pro Leu Phe Leu Leu Cys Pro Ser Phe Ser Ile Arg  
35 40 45  
Glu Gln Arg Asp Phe Ser Glu Ser Arg Glu His Leu Ala Arg Gln Leu  
50 55 60  
Thr Ser Thr Ser Phe Gln Pro Glu Pro Ala Gln Val Trp Glu Gly Ala  
65 70 75 80  
Ser Trp Pro Pro Pro Arg Cys Ser Ser Pro Ser Ser Leu Pro Pro Pro  
85 90 95  
Ser Leu Pro Pro Phe Pro Pro Arg Ser Asp Gln Phe Leu Ser Leu Pro  
100 105 110  
Ser Pro Gln Ala Gln  
115

<210> 55  
<211> 1763  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS

<222> (26)..(922)

<400> 55

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			Met	Ala	Ala	Arg	Arg	Ala	Leu	His	Phe					
			1				5									
gta	ttc	aaa	gtg	gga	aac	cgc	ttc	cag	acg	gcg	cgt	ttc	tat	cgg	gac	100
Val	Phe	Lys	Val	Gly	Asn	Arg	Phe	Gln	Thr	Ala	Arg	Phe	Tyr	Arg	Asp	
10				15						20					25	
gtc	ctg	ggg	atg	aag	gtt	ctg	cgg	cat	gag	gaa	ttt	gaa	gaa	ggc	tgc	148
Val	Leu	Gly	Met	Lys	Val	Leu	Arg	His	Glu	Glu	Phe	Glu	Glu	Gly	Cys	
				30					35					40		
aaa	gct	gcc	tgt	aat	ggg	cct	tat	gat	ggg	aaa	tgg	agt	aaa	aca	atg	196
Lys	Ala	Ala	Cys	Asn	Gly	Pro	Tyr	Asp	Gly	Lys	Trp	Ser	Lys	Thr	Met	
			45					50					55			
gtg	gga	ttt	ggg	cct	gag	gat	gat	cat	ttt	gtc	gca	gaa	ctg	act	tac	244
Val	Gly	Phe	Gly	Pro	Glu	Asp	Asp	His	Phe	Val	Ala	Glu	Leu	Thr	Tyr	
	60						65					70				
aat	tat	ggc	gtc	gga	gac	tac	aag	ctt	ggc	aat	gac	ttt	atg	gga	atc	292
Asn	Tyr	Gly	Val	Gly	Asp	Tyr	Lys	Leu	Gly	Asn	Asp	Phe	Met	Gly	Ile	
	75					80					85					
acg	ctc	gct	tct	agc	cag	gct	gtc	agc	aac	gcc	agg	aag	ctg	gag	tgg	340
Thr	Leu	Ala	Ser	Ser	Gln	Ala	Val	Ser	Asn	Ala	Arg	Lys	Leu	Glu	Trp	
90					95					100					105	
cca	ctg	acg	gaa	gtt	gca	gaa	ggg	gtt	ttt	gaa	acc	gag	gcc	ccg	gga	388
Pro	Leu	Thr	Glu	Val	Ala	Glu	Gly	Val	Phe	Glu	Thr	Glu	Ala	Pro	Gly	
				110					115					120		
gga	tat	aag	ttc	tat	ttg	cag	aat	cgc	agt	ctg	cct	cag	tca	gat	cct	436
Gly	Tyr	Lys	Phe	Tyr	Leu	Gln	Asn	Arg	Ser	Leu	Pro	Gln	Ser	Asp	Pro	
			125					130					135			
gta	tta	aaa	gta	act	cta	gca	gtg	tct	gat	ctt	caa	aag	tcc	ttg	aac	484
Val	Leu	Lys	Val	Thr	Leu	Ala	Val	Ser	Asp	Leu	Gln	Lys	Ser	Leu	Asn	
	140						145					150				
tac	tgg	tgt	aat	cta	ctg	gga	atg	aaa	att	tat	gaa	aaa	gat	gaa	gaa	532
Tyr	Trp	Cys	Asn	Leu	Leu	Gly	Met	Lys	Ile	Tyr	Glu	Lys	Asp	Glu	Glu	
	155					160					165					
aag	caa	agg	gct	ttg	ctg	ggc	tat	gct	gat	aac	cag	tgt	aag	ctg	gag	580
Lys	Gln	Arg	Ala	Leu	Leu	Gly	Tyr	Ala	Asp	Asn	Gln	Cys	Lys	Leu	Glu	
170					175					180					185	
cta	cag	ggc	gtc	aag	ggg	ggg	gtg	gac	cat	gca	gca	gct	ttt	gga	aga	628
Leu	Gln	Gly	Val	Lys	Gly	Gly	Val	Asp	His	Ala	Ala	Ala	Phe	Gly	Arg	
				190					195					200		
att	gcc	ttc	tct	tgc	ccc	cag	aaa	gag	ttg	cca	gac	tta	gaa	gac	ttg	676
Ile	Ala	Phe	Ser	Cys	Pro	Gln	Lys	Glu	Leu	Pro	Asp	Leu	Glu	Asp	Leu	

09890688-092701

205	210	215	
atg aaa agg gag aac cag aag att ctg act ccc ctg gtg agc ctg gac			724
Met Lys Arg Glu Asn Gln Lys Ile Leu Thr Pro Leu Val Ser Leu Asp			
220	225	230	
acc cca ggg aaa gca aca gta cag gtg gtc att ctg gcc gac cct gac			772
Thr Pro Gly Lys Ala Thr Val Gln Val Val Ile Leu Ala Asp Pro Asp			
235	240	245	
gga cat gaa att tgc ttt gtc ggg gat gaa gca ttt cga gaa ctt tct			820
Gly His Glu Ile Cys Phe Val Gly Asp Glu Ala Phe Arg Glu Leu Ser			
250	255	260	265
aag atg gat cca gag gga agc aaa ttg ttg gat gat gca atg gca gca			868
Lys Met Asp Pro Glu Gly Ser Lys Leu Leu Asp Asp Ala Met Ala Ala			
270	275	280	
gat aaa agt gac gag tgg ttt gcc aaa cac aat aaa ccc aaa gct tca			916
Asp Lys Ser Asp Glu Trp Phe Ala Lys His Asn Lys Pro Lys Ala Ser			
285	290	295	
ggt taa cggaagacat gatgcagagc aagcctctgt gattcctgcc cagcacctgt			972
Gly			
gaggcctgac gtgtcagttc ccaataaatg ctcttctgat ttgtttcccg tacaggcaag			1032
gaggcttggg tagtgcatgt ttgtgtatatt caatctttga aagctctgat gtaatttaga			1092
aatgaaatcc aatcatgagt ccaggtagag aacgcctgct gtaatctaca ctgttgctgg			1152
gactgcgcat tctgtatata actgtgttgg atgagtgaca gatgattgtc cagactagga			1212
cagcggcatg aacatgactt tgggtgggat tgcggatagt tagggttacc tctgaatcgt			1272
gtagctttta tgagagcagc tgtgcaagtg aatccacatt aatgccttgt cgtgggtgcc			1332
ttcccagcgc ctgacgatac gctcttctat tgtcttattc tggcagggtt tgacgtttta			1392
aattttttta agaaatttta ttccctggac caaaagggtt ggttaaccac cccctctta			1452
cttgctttca cattttgagt gtccagagga aacagaaagg aatgagtgtg tgacgttgct			1512
gcacgcctga ctctgtgcga gcttctttct gtgtatatat tttgttttat tttttccgt			1572
gtatatTTTT aatcccgaca gaacatcatg tgagatttct ttaaaatgga ttaaacgatt			1632
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<210> 56  
 <211> 298  
 <212> PRT

098906888 - 092701

<213> Homo sapiens

<400> 56

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Arg His Glu Glu Phe Glu Glu Gly Cys Lys Ala Ala Cys Asn Gly Pro
          35          40          45
Tyr Asp Gly Lys Trp Ser Lys Thr Met Val Gly Phe Gly Pro Glu Asp
          50          55          60
Asp His Phe Val Ala Glu Leu Thr Tyr Asn Tyr Gly Val Gly Asp Tyr
          65          70          75          80
Lys Leu Gly Asn Asp Phe Met Gly Ile Thr Leu Ala Ser Ser Gln Ala
          85          90          95
Val Ser Asn Ala Arg Lys Leu Glu Trp Pro Leu Thr Glu Val Ala Glu
          100          105          110
Gly Val Phe Glu Thr Glu Ala Pro Gly Gly Tyr Lys Phe Tyr Leu Gln
          115          120          125
Asn Arg Ser Leu Pro Gln Ser Asp Pro Val Leu Lys Val Thr Leu Ala
          130          135          140
Val Ser Asp Leu Gln Lys Ser Leu Asn Tyr Trp Cys Asn Leu Leu Gly
          145          150          155          160
Met Lys Ile Tyr Glu Lys Asp Glu Glu Lys Gln Arg Ala Leu Leu Gly
          165          170          175
Tyr Ala Asp Asn Gln Cys Lys Leu Glu Leu Gln Gly Val Lys Gly Gly
          180          185          190
Val Asp His Ala Ala Ala Phe Gly Arg Ile Ala Phe Ser Cys Pro Gln
          195          200          205
Lys Glu Leu Pro Asp Leu Glu Asp Leu Met Lys Arg Glu Asn Gln Lys
          210          215          220
Ile Leu Thr Pro Leu Val Ser Leu Asp Thr Pro Gly Lys Ala Thr Val
          225          230          235          240
Gln Val Val Ile Leu Ala Asp Pro Asp Gly His Glu Ile Cys Phe Val
          245          250          255
Gly Asp Glu Ala Phe Arg Glu Leu Ser Lys Met Asp Pro Glu Gly Ser
          260          265          270
Lys Leu Leu Asp Asp Ala Met Ala Ala Asp Lys Ser Asp Glu Trp Phe
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Ala Lys His Asn Lys Pro Lys Ala Ser Gly
          290          295

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<210> 57

<211> 1913

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (303)..(1379)

<400> 57

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gagactgtcc gaagactgct atctgggacg agacaagttg ttaaaggac aggagagaaa 180  
gcagagctat ttcaagagtg agccacagaa gggaatccag aggccatcta agcgaggaag 240  
ggtctacagg cagtgagtga aggccaggag cagggcccag gccaggcacg accaccgagg 300  
gg atg aac ttc aca gtg ggt ttc aag ccg ctg cta ggg gat gca cac 347  
Met Asn Phe Thr Val Gly Phe Lys Pro Leu Leu Gly Asp Ala His  
1 5 10 15  
agc atg gac aac ctg gag aag cag ctc atc tgc ccc atc tgc ctg gag 395  
Ser Met Asp Asn Leu Glu Lys Gln Leu Ile Cys Pro Ile Cys Leu Glu  
20 25 30  
atg ttc tcc aaa cca gtg gtg atc ctg ccc tgc caa cac aac ctg tgc 443  
Met Phe Ser Lys Pro Val Val Ile Leu Pro Cys Gln His Asn Leu Cys  
35 40 45  
cgc aaa tgt gcc aac gac gtc ttc cag gcc tcg aat cct cta tgg cag 491  
Arg Lys Cys Ala Asn Asp Val Phe Gln Ala Ser Asn Pro Leu Trp Gln  
50 55 60  
tcc cgg ggc tcc acc act gtg tct tca gga ggc cgt ttc cgc tgc cca 539  
Ser Arg Gly Ser Thr Thr Val Ser Ser Gly Gly Arg Phe Arg Cys Pro  
65 70 75  
tcg tgc agg cat gag gtt gtc ctg gac aga cac ggt gtc tac ggc ctg 587  
Ser Cys Arg His Glu Val Val Leu Asp Arg His Gly Val Tyr Gly Leu  
80 85 90 95  
cag cga aac ctg cta gtg gag aac att atc gac att tac aag cag gag 635  
Gln Arg Asn Leu Val Glu Asn Ile Ile Asp Ile Tyr Lys Gln Glu  
100 105 110  
tca tcc agg ccg ctg cac tcc aag gct gag cag cac ctc atg tgc gag 683  
Ser Ser Arg Pro Leu His Ser Lys Ala Glu Gln His Leu Met Cys Glu  
115 120 125  
gag cat gaa gaa gag aag atc aat att tac tgc ctg agc tgt gag gtg 731  
Glu His Glu Glu Glu Lys Ile Asn Ile Tyr Cys Leu Ser Cys Glu Val  
130 135 140  
ccc acc tgc tct ctc tgc aag gtc ttc ggt gcc cac aag gac tgt gag 779  
Pro Thr Cys Ser Leu Cys Lys Val Phe Gly Ala His Lys Asp Cys Glu  
145 150 155  
gtg gcc cca ctg ccc acc att tac aaa cgc cag aag agt gag ctc agc 827  
Val Ala Pro Leu Pro Thr Ile Tyr Lys Arg Gln Lys Ser Glu Leu Ser  
160 165 170 175  
gat ggc atc gcg atg ctg gtg gca ggc aat gac cgc gtg caa gca gtg 875  
Asp Gly Ile Ala Met Leu Val Ala Gly Asn Asp Arg Val Gln Ala Val  
180 185 190  
atc aca cag atg gag gag gtg tgc cag act atc gag gac aat agc cgg 923  
Ile Thr Gln Met Glu Glu Val Cys Gln Thr Ile Glu Asp Asn Ser Arg



195	200	205	
agg cag aag cag ttg tta aac cag agg ttt gag agc ctg tgc gca gtg Arg Gln Lys Gln Leu Leu Asn Gln Arg Phe Glu Ser Leu Cys Ala Val 210 215 220			971
ctg gag gag cgc aag ggt gag ctg ctg cag gcg ctg gcc cgg gag caa Leu Glu Glu Arg Lys Gly Glu Leu Leu Gln Ala Leu Ala Arg Glu Gln 225 230 235			1019
gag gag aag ctg cag cgc gtc cgc ggc ctc atc cgt cag tat ggc gac Glu Glu Lys Leu Gln Arg Val Arg Gly Leu Ile Arg Gln Tyr Gly Asp 240 245 250 255			1067
cac ctg gag gcc tcc tct aag ctg gtg gag tct gcc atc cag tcc atg His Leu Glu Ala Ser Ser Lys Leu Val Glu Ser Ala Ile Gln Ser Met 260 265 270			1115
gaa gag cca caa atg gcg ctg tat ctc cag cag gcc aag gag ctg atc Glu Glu Pro Gln Met Ala Leu Tyr Leu Gln Gln Ala Lys Glu Leu Ile 275 280 285			1163
aat aag gtc ggg gcc atg tcg aag gtg gag ctg gca ggg cgg ccg gag Asn Lys Val Gly Ala Met Ser Lys Val Glu Leu Ala Gly Arg Pro Glu 290 295 300			1211
cca ggc tat gag agc atg gag caa ttc acc gta agg gtg gag cac gtg Pro Gly Tyr Glu Ser Met Glu Gln Phe Thr Val Arg Val Glu His Val 305 310 315			1259
gcc gaa atg ctg cgg acc atc gac ttc cag cca ggc gct tcc ggg gag Ala Glu Met Leu Arg Thr Ile Asp Phe Gln Pro Gly Ala Ser Gly Glu 320 325 330 335			1307
gaa gag gag gtg gcc cca gac gga gag gag ggc agc gcg ggg ccg gag Glu Glu Glu Val Ala Pro Asp Gly Glu Glu Gly Ser Ala Gly Pro Glu 340 345 350			1355
gaa gag cgg ccg gat ggg cct taa ggccctgcgcc gacccgaccc tgctcgagag Glu Glu Arg Pro Asp Gly Pro 355			1409
cccgcgctag agtcgggggag gatctgcgca gagaccgcag catcacccaa atcggcgccg			1469
gccccgggag gatctcaata aagaactcga gcgtcccaga cccgtatctc ctttcgctgc			1529
ccaaccccgcc agcctggggt tcgaaggcga cccgcccacc atcctgccct tcccagaacc			1589
tgagaccgtc tggggggcgag aagccaaatg aaccctatt gggcacctct gtgatgccag			1649
gagcgaactg gtgagcccag cgccctggga agagggccga gggcggggcg gtggtgccgg			1709
gacctctgag gtccctgggga tttggggacc cttgggggtcc acatgcacct ggctgacctg			1769
gctgaaagcc gctgtctcgg agccccccac agcattttgt tcccctcccg ctggccccggg			1829
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1913

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 <212> PRT  
 <213> Homo sapiens

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 Phe Ser Lys Pro Val Val Ile Leu Pro Cys Gln His Asn Leu Cys Arg  
 35 40 45  
 Lys Cys Ala Asn Asp Val Phe Gln Ala Ser Asn Pro Leu Trp Gln Ser  
 50 55 60  
 Arg Gly Ser Thr Thr Val Ser Ser Gly Gly Arg Phe Arg Cys Pro Ser  
 65 70 75 80  
 Cys Arg His Glu Val Val Leu Asp Arg His Gly Val Tyr Gly Leu Gln  
 85 90 95  
 Arg Asn Leu Leu Val Glu Asn Ile Ile Asp Ile Tyr Lys Gln Glu Ser  
 100 105 110  
 Ser Arg Pro Leu His Ser Lys Ala Glu Gln His Leu Met Cys Glu Glu  
 115 120 125  
 His Glu Glu Glu Lys Ile Asn Ile Tyr Cys Leu Ser Cys Glu Val Pro  
 130 135 140  
 Thr Cys Ser Leu Cys Lys Val Phe Gly Ala His Lys Asp Cys Glu Val  
 145 150 155 160  
 Ala Pro Leu Pro Thr Ile Tyr Lys Arg Gln Lys Ser Glu Leu Ser Asp  
 165 170 175  
 Gly Ile Ala Met Leu Val Ala Gly Asn Asp Arg Val Gln Ala Val Ile  
 180 185 190  
 Thr Gln Met Glu Glu Val Cys Gln Thr Ile Glu Asp Asn Ser Arg Arg  
 195 200 205  
 Gln Lys Gln Leu Leu Asn Gln Arg Phe Glu Ser Leu Cys Ala Val Leu  
 210 215 220  
 Glu Glu Arg Lys Gly Glu Leu Leu Gln Ala Leu Ala Arg Glu Gln Glu  
 225 230 235 240  
 Glu Lys Leu Gln Arg Val Arg Gly Leu Ile Arg Gln Tyr Gly Asp His  
 245 250 255  
 Leu Glu Ala Ser Ser Lys Leu Val Glu Ser Ala Ile Gln Ser Met Glu  
 260 265 270  
 Glu Pro Gln Met Ala Leu Tyr Leu Gln Gln Ala Lys Glu Leu Ile Asn  
 275 280 285  
 Lys Val Gly Ala Met Ser Lys Val Glu Leu Ala Gly Arg Pro Glu Pro  
 290 295 300  
 Gly Tyr Glu Ser Met Glu Gln Phe Thr Val Arg Val Glu His Val Ala  
 305 310 315 320  
 Glu Met Leu Arg Thr Ile Asp Phe Gln Pro Gly Ala Ser Gly Glu Glu  
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 Glu Arg Pro Asp Gly Pro  
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09390688-092701

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 <222> (32)..(1147)

<400> 59

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Gly Phe Ala Arg Gly Leu Arg Ala Leu Ala Leu Ala Trp Leu Pro Gly
          10           15           20

tgg cgg ggc cgc tcc ttc gcc ctg gcg cgt gcg gca ggc gcg ccc cac      148
Trp Arg Gly Arg Ser Phe Ala Leu Ala Arg Ala Ala Gly Ala Pro His
          25           30           35

ggg ggt gac ttg cag ccc ccc gcc tgt ccc gag ccg cgc ggg cgc cag      196
Gly Gly Asp Leu Gln Pro Pro Ala Cys Pro Glu Pro Arg Gly Arg Gln
          40           45           50           55

ctc agt ttg tcc gcg gcg gcg gtg gtg gac tct gcg ccc cgc ccc ctg      244
Leu Ser Leu Ser Ala Ala Ala Val Val Asp Ser Ala Pro Arg Pro Leu
          60           65           70

cag ccg tac ttg cgc ctc atg cgg ttg gac aag ccc att gga acc tgg      292
Gln Pro Tyr Leu Arg Leu Met Arg Leu Asp Lys Pro Ile Gly Thr Trp
          75           80           85

ctt ctg tat tta cca tgt acc tgg agc att ggt ttg gca gct gaa cca      340
Leu Leu Tyr Leu Pro Cys Thr Trp Ser Ile Gly Leu Ala Ala Glu Pro
          90           95           100

ggg tgt ttt cca gat tgg tac atg ctc tcc ctc ttt ggc act gga gct      388
Gly Cys Phe Pro Asp Trp Tyr Met Leu Ser Leu Phe Gly Thr Gly Ala
          105           110           115

att ctg atg cgt gga gca ggc tgt act att aat gac atg tgg gac cag      436
Ile Leu Met Arg Gly Ala Gly Cys Thr Ile Asn Asp Met Trp Asp Gln
          120           125           130           135

gac tat gat aaa aag gtt aca aga aca gcc aat cgt cca ata gcc gct      484
Asp Tyr Asp Lys Lys Val Thr Arg Thr Ala Asn Arg Pro Ile Ala Ala
          140           145           150

gga gac att tca act ttt cag tcc ttt gtt ttt ctt ggg gga cag cta      532
Gly Asp Ile Ser Thr Phe Gln Ser Phe Val Phe Leu Gly Gly Gln Leu
          155           160           165

acc ctg gca ctg ggt gtt ctt ctg tgt cta aat tac tac agt ata gct      580
Thr Leu Ala Leu Gly Val Leu Leu Cys Leu Asn Tyr Tyr Ser Ile Ala

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09390688.092701

170	175	180	
ctg gga gca gga tcc tta ctt ctt gtc atc acc tac cca cta atg aaa			628
Leu Gly Ala Gly Ser Leu Leu Leu Val Ile Thr Tyr Pro Leu Met Lys			
185	190	195	
aga att tca tac tgg cct caa cta gcc ttg ggc ttg aca ttt aat tgg			676
Arg Ile Ser Tyr Trp Pro Gln Leu Ala Leu Gly Leu Thr Phe Asn Trp			
200	205	210	215
gga gcg tta ctt gga tgg tct gct atc aag ggt tcc tgt gat cca tct			724
Gly Ala Leu Leu Gly Trp Ser Ala Ile Lys Gly Ser Cys Asp Pro Ser			
220	225	230	
gtt tgc ctg cct ctt tat ttt tct gga gtt atg tgg aca cta ata tat			772
Val Cys Leu Pro Leu Tyr Phe Ser Gly Val Met Trp Thr Leu Ile Tyr			
235	240	245	
gac act att tat gcc cat cag gac aaa aga gat gat gtt ttg att ggt			820
Asp Thr Ile Tyr Ala His Gln Asp Lys Arg Asp Asp Val Leu Ile Gly			
250	255	260	
ctt aag tca acg gct ctg cgg ttc gga gaa aat acc aag ccg tgg ctc			868
Leu Lys Ser Thr Ala Leu Arg Phe Gly Glu Asn Thr Lys Pro Trp Leu			
265	270	275	
agc gcc ttc agt gtt gca atg ctg ggg gca ctg agc cta gtg ggt gtg			916
Ser Gly Phe Ser Val Ala Met Leu Gly Ala Leu Ser Leu Val Gly Val			
280	285	290	295
aac agt gga cag act gct ccc tac tac gct gcc ctg ggt gct gta gga			964
Asn Ser Gly Gln Thr Ala Pro Tyr Tyr Ala Ala Leu Gly Ala Val Gly			
300	305	310	
gcc cat ctg act cac cag att tac act cta gac atc cac aga cct gag			1012
Ala His Leu Thr His Gln Ile Tyr Thr Leu Asp Ile His Arg Pro Glu			
315	320	325	
gat tgt tgg aat aaa ttt atc tcc aac cga aca ctg gga cta ata gtt			1060
Asp Cys Trp Asn Lys Phe Ile Ser Asn Arg Thr Leu Gly Leu Ile Val			
330	335	340	
ttt tta ggg att gtc ctt ggg aat ttg tgg aaa gaa aag aag aca gac			1108
Phe Leu Gly Ile Val Leu Gly Asn Leu Trp Lys Glu Lys Lys Thr Asp			
345	350	355	
aaa aca aag aag ggt ata gag aat aaa ata gaa aat taa tgaatgaaat			1157
Lys Thr Lys Lys Gly Ile Glu Asn Lys Ile Glu Asn			
360	365	370	
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gatacaatat gttaaagaat taagaacctg aagatgaaga tttagagcat atttacctgg			1277
attttactta tttgctagca aaattccccc ttgtcacaga aaccagggac tcttcaggat			1337
ttgagatggc cttgagtatt ttagttgata cattcttctg cccattataa ttctcacctg			1397

aagttatggg gattgcacag gttttggcac tttagaaaaa gcctgatgtg ggtcttacat 1457  
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 Arg Ala Ala Gly Ala Pro His Gly Gly Asp Leu Gln Pro Ala Cys  
 35 40 45  
 Pro Glu Pro Arg Gly Arg Gln Leu Ser Leu Ser Ala Ala Val Val  
 50 55 60  
 Asp Ser Ala Pro Arg Pro Leu Gln Pro Tyr Leu Arg Leu Met Arg Leu  
 65 70 75 80  
 Asp Lys Pro Ile Gly Thr Trp Leu Leu Tyr Leu Pro Cys Thr Trp Ser  
 85 90 95  
 Ile Gly Leu Ala Ala Glu Pro Gly Cys Phe Pro Asp Trp Tyr Met Leu  
 100 105 110  
 Ser Leu Phe Gly Thr Gly Ala Ile Leu Met Arg Gly Ala Gly Cys Thr  
 115 120 125  
 Ile Asn Asp Met Trp Asp Gln Asp Tyr Asp Lys Lys Val Thr Arg Thr  
 130 135 140  
 Ala Asn Arg Pro Ile Ala Ala Gly Asp Ile Ser Thr Phe Gln Ser Phe  
 145 150 155 160  
 Val Phe Leu Gly Gly Gln Leu Thr Leu Ala Leu Gly Val Leu Leu Cys  
 165 170 175  
 Leu Asn Tyr Tyr Ser Ile Ala Leu Gly Ala Gly Ser Leu Leu Leu Val  
 180 185 190  
 Ile Thr Tyr Pro Leu Met Lys Arg Ile Ser Tyr Trp Pro Gln Leu Ala  
 195 200 205  
 Leu Gly Leu Thr Phe Asn Trp Gly Ala Leu Leu Gly Trp Ser Ala Ile  
 210 215 220  
 Lys Gly Ser Cys Asp Pro Ser Val Cys Leu Pro Leu Tyr Phe Ser Gly  
 225 230 235 240  
 Val Met Trp Thr Leu Ile Tyr Asp Thr Ile Tyr Ala His Gln Asp Lys  
 245 250 255  
 Arg Asp Asp Val Leu Ile Gly Leu Lys Ser Thr Ala Leu Arg Phe Gly  
 260 265 270  
 Glu Asn Thr Lys Pro Trp Leu Ser Gly Phe Ser Val Ala Met Leu Gly  
 275 280 285  
 Ala Leu Ser Leu Val Gly Val Asn Ser Gly Gln Thr Ala Pro Tyr Tyr  
 290 295 300  
 Ala Ala Leu Gly Ala Val Gly Ala His Leu Thr His Gln Ile Tyr Thr  
 305 310 315 320  
 Leu Asp Ile His Arg Pro Glu Asp Cys Trp Asn Lys Phe Ile Ser Asn  
 325 330 335  
 Arg Thr Leu Gly Leu Ile Val Phe Leu Gly Ile Val Leu Gly Asn Leu

09890688-092701

340 345 350  
 Trp Lys Glu Lys Lys Thr Asp Lys Thr Lys Lys Gly Ile Glu Asn Lys  
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 Ile Glu Asn  
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 <212> DNA  
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<220>  
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 <222> (183)..(1301)

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 cagcattgtg ttagtgccgc gagggccactg tgtcagcaag ctgagaggga aactgaagca 180  
 ag atg tcg ggc cgg agt ggg aag aag aaa atg tcc aag ctg tcc cgt 227  
 Met Ser Gly Arg Ser Gly Lys Lys Lys Met Ser Lys Leu Ser Arg  
 1 5 10 15  
 tca gct agg gca ggt gtc atc ttt cca gtg ggg agg ctg atg cgt tat 275  
 Ser Ala Arg Ala Gly Val Ile Phe Pro Val Gly Arg Leu Met Arg Tyr  
 20 25 30  
 ctg aag aaa ggg acg ttc aag tac cgg atc agc gtg ggc gcc cct gtc 323  
 Leu Lys Lys Gly Thr Phe Lys Tyr Arg Ile Ser Val Gly Ala Pro Val  
 35 40 45  
 tac atg gcg gca gtc att gag tac ctg gca gcg gaa att cta gaa ttg 371  
 Tyr Met Ala Ala Val Ile Glu Tyr Leu Ala Ala Glu Ile Leu Glu Leu  
 50 55 60  
 gcc ggc aat gcc gcg agg gac aac aag aag gcc cgg ata gcc ccg aga 419  
 Ala Gly Asn Ala Ala Arg Asp Asn Lys Lys Ala Arg Ile Ala Pro Arg  
 65 70 75  
 cac atc ttg ctg gca gtt gcc aat gac gag gag ctc aac cag ctg cta 467  
 His Ile Leu Leu Ala Val Ala Asn Asp Glu Glu Leu Asn Gln Leu Leu  
 80 85 90 95  
 aaa gga gtg acc atc gcc agt gga ggc gtc ctg ccc aga att cac ccc 515  
 Lys Gly Val Thr Ile Ala Ser Gly Gly Val Leu Pro Arg Ile His Pro  
 100 105 110  
 gaa ctg ctg gcc aaa aag cga ggg acc aaa ggc aag tcg gaa acg atc 563  
 Glu Leu Leu Ala Lys Lys Arg Gly Thr Lys Gly Lys Ser Glu Thr Ile  
 115 120 125  
 ctc tcc cca ccc cca gag aaa aga ggc agg aag gcc acg tca ggc aag 611

09890688.092701

Leu	Ser	Pro	Pro	Pro	Glu	Lys	Arg	Gly	Arg	Lys	Ala	Thr	Ser	Gly	Lys		
		130					135					140					
aag	ggg	ggg	aag	aaa	tcc	aag	gct	gcc	aaa	cca	cgg	acg	tcc	aaa	aag	659	
Lys	Gly	Gly	Lys	Lys	Ser	Lys	Ala	Ala	Lys	Pro	Arg	Thr	Ser	Lys	Lys		
	145					150				155							
tcc	aaa	cca	aag	gac	agc	gat	aaa	gaa	gga	act	tca	aat	tcc	acc	tct	707	
Ser	Lys	Pro	Lys	Asp	Ser	Asp	Lys	Glu	Gly	Thr	Ser	Asn	Ser	Thr	Ser		
160					165					170					175		
gaa	gat	ggg	cca	ggg	gat	gga	ttc	acc	att	ctg	tct	tct	aag	agc	ctt	755	
Glu	Asp	Gly	Pro	Gly	Asp	Gly	Phe	Thr	Ile	Leu	Ser	Ser	Lys	Ser	Leu		
				180					185					190			
gtt	ctg	gga	cag	aag	ctg	tcc	tta	acc	cag	agt	gac	atc	agc	cat	att	803	
Val	Leu	Gly	Gln	Lys	Leu	Ser	Leu	Thr	Gln	Ser	Asp	Ile	Ser	His	Ile		
			195					200					205				
ggc	tcc	atg	aga	gtg	gag	ggc	att	gtc	cac	cca	acc	aca	gcc	gaa	att	851	
Gly	Ser	Met	Arg	Val	Glu	Gly	Ile	Val	His	Pro	Thr	Thr	Ala	Glu	Ile		
		210					215					220					
gac	ctc	aaa	gaa	gat	ata	ggc	aaa	gcc	ttg	gaa	aag	gct	ggg	gga	aaa	899	
Asp	Leu	Lys	Glu	Asp	Ile	Gly	Lys	Ala	Leu	Glu	Lys	Ala	Gly	Gly	Lys		
	225					230					235						
gag	ttc	ttg	gaa	acg	gta	aag	gag	ctt	cgc	aaa	tcc	caa	ggc	cct	ttg	947	
Glu	Phe	Leu	Glu	Thr	Val	Lys	Glu	Leu	Arg	Lys	Ser	Gln	Gly	Pro	Leu		
240					245				250						255		
gaa	gtc	gcc	gaa	gcc	gcc	gtc	agc	caa	tcc	agt	gga	ctc	gca	gcc	aaa	995	
Glu	Val	Ala	Glu	Ala	Ala	Val	Ser	Gln	Ser	Ser	Gly	Leu	Ala	Ala	Lys		
				260				265						270			
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Phe	Val	Ile	His	Cys	His	Ile	Pro	Gln	Trp	Gly	Ser	Asp	Lys	Cys	Glu		
			275					280					285				
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Glu	Gln	Leu	Glu	Glu	Thr	Ile	Lys	Asn	Cys	Leu	Ser	Ala	Ala	Glu	Asp		
		290					295					300					
aag	aag	cta	aag	tcc	gtc	gcg	ttc	ccg	cct	ttc	ccc	agc	ggc	aga	aac	1139	
Lys	Lys	Leu	Lys	Ser	Val	Ala	Phe	Pro	Pro	Phe	Pro	Ser	Gly	Arg	Asn		
		305				310					315						
tgc	ttt	ccc	aaa	cag	act	gcg	gcc	cag	gtg	acc	ctc	aaa	gcc	atc	tca	1187	
Cys	Phe	Pro	Lys	Gln	Thr	Ala	Ala	Gln	Val	Thr	Leu	Lys	Ala	Ile	Ser		
320					325					330					335		
gcc	cac	ttt	gat	gac	tcg	agc	gcg	tcc	tcg	ctg	aag	aac	gtg	tac	ttc	1235	
Ala	His	Phe	Asp	Asp	Ser	Ser	Ala	Ser	Ser	Leu	Lys	Asn	Val	Tyr	Phe		
				340				345						350			
ctg	ctc	ttc	gac	agc	gag	agc	atc	ggc	atc	tac	gtg	cag	gag	atg	gcc	1283	
Leu	Leu	Phe	Asp	Ser	Glu	Ser	Ile	Gly	Ile	Tyr	Val	Gln	Glu	Met	Ala		

09890688-092701

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355              360              365
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Lys Leu Asp Ala Lys
370

cgacccgagt cccaagagtg gggttttgct ttttaaaagg agagaggagg ggtgatggca 1391
ggggagtgga ggggtggcgg gcaggtcctg ccggcgcagg gagccctctg cccttcacac 1451
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      35              40              45
Met Ala Ala Val Ile Glu Tyr Leu Ala Ala Glu Ile Leu Glu Leu Ala
      50              55              60
Gly Asn Ala Ala Arg Asp Asn Lys Lys Ala Arg Ile Ala Pro Arg His
      65              70              75              80
Ile Leu Leu Ala Val Ala Asn Asp Glu Glu Leu Asn Gln Leu Leu Lys
      85              90              95
Gly Val Thr Ile Ala Ser Gly Gly Val Leu Pro Arg Ile His Pro Glu
      100             105             110
Leu Leu Ala Lys Lys Arg Gly Thr Lys Gly Lys Ser Glu Thr Ile Leu
      115             120             125
Ser Pro Pro Pro Glu Lys Arg Gly Arg Lys Ala Thr Ser Gly Lys Lys
      130             135             140
Gly Gly Lys Lys Ser Lys Ala Ala Lys Pro Arg Thr Ser Lys Lys Ser
      145             150             155             160
Lys Pro Lys Asp Ser Asp Lys Glu Gly Thr Ser Asn Ser Thr Ser Glu
      165             170             175
Asp Gly Pro Gly Asp Gly Phe Thr Ile Leu Ser Ser Lys Ser Leu Val
      180             185             190
Leu Gly Gln Lys Leu Ser Leu Thr Gln Ser Asp Ile Ser His Ile Gly
      195             200             205
Ser Met Arg Val Glu Gly Ile Val His Pro Thr Thr Ala Glu Ile Asp
      210             215             220
Leu Lys Glu Asp Ile Gly Lys Ala Leu Glu Lys Ala Gly Gly Lys Glu
      225             230             235             240

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Phe Leu Glu Thr Val Lys Glu Leu Arg Lys Ser Gln Gly Pro Leu Glu  
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 Val Ala Glu Ala Ala Val Ser Gln Ser Ser Gly Leu Ala Ala Lys Phe  
 260 265 270  
 Val Ile His Cys His Ile Pro Gln Trp Gly Ser Asp Lys Cys Glu Glu  
 275 280 285  
 Gln Leu Glu Glu Thr Ile Lys Asn Cys Leu Ser Ala Ala Glu Asp Lys  
 290 295 300  
 Lys Leu Lys Ser Val Ala Phe Pro Pro Phe Pro Ser Gly Arg Asn Cys  
 305 310 315 320  
 Phe Pro Lys Gln Thr Ala Ala Gln Val Thr Leu Lys Ala Ile Ser Ala  
 325 330 335  
 His Phe Asp Asp Ser Ser Ala Ser Ser Leu Lys Asn Val Tyr Phe Leu  
 340 345 350  
 Leu Phe Asp Ser Glu Ser Ile Gly Ile Tyr Val Gln Glu Met Ala Lys  
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 Leu Asp Ala Lys  
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 Ser Leu Asn Leu Ala Pro Pro Thr Val Ala Ala Pro Ala Pro Ser Leu  
 15 20 25

ttc ccc gcc gcc cag atg atg aac aat ggc ctc ctc caa cag ccc tct 149  
 Phe Pro Ala Ala Gln Met Met Asn Asn Gly Leu Leu Gln Gln Pro Ser  
 30 35 40

gcc ttg atg ttg ctc ccc tgc cgc cca gtt ctt act tct gtg gcc ctt 197  
 Ala Leu Met Leu Leu Pro Cys Arg Pro Val Leu Thr Ser Val Ala Leu  
 45 50 55

aat gcc aac ttt gtg tcc tgg aag agt cgt acc aag tac acc att aca 245  
 Asn Ala Asn Phe Val Ser Trp Lys Ser Arg Thr Lys Tyr Thr Ile Thr  
 60 65 70 75

cca gtg aag atg agg aag tct ggg ggc cga gac cac aca ggc cga atc 293  
 Pro Val Lys Met Arg Lys Ser Gly Gly Arg Asp His Thr Gly Arg Ile  
 80 85 90

cgg gtg cat ggt att ggc ggg ggc cac aag caa cgt tat cga atg att 341  
 Arg Val His Gly Ile Gly Gly Gly His Lys Gln Arg Tyr Arg Met Ile

95	100	105	
gac ttt ctg cgt ttc cgg cct gag gag acc aag tca gga ccc ttt gag			389
Asp Phe Leu Arg Phe Arg Pro Glu Glu Thr Lys Ser Gly Pro Phe Glu			
110	115	120	
gag aag gtt atc caa gtc cgc tat gat ccc tgt agg tca gca gac ata			437
Glu Lys Val Ile Gln Val Arg Tyr Asp Pro Cys Arg Ser Ala Asp Ile			
125	130	135	
gct ctg gtt gct ggg ggc agc cgg aaa cgc tgg atc atc gcc aca gaa			485
Ala Leu Val Ala Gly Gly Ser Arg Lys Arg Trp Ile Ile Ala Thr Glu			
140	145	150	155
aac atg cag gct gga gat aca atc ttg aac tct aac cac ata ggc cga			533
Asn Met Gln Ala Gly Asp Thr Ile Leu Asn Ser Asn His Ile Gly Arg			
160	165	170	
atg gca gtt gct gct cgg gaa ggg gat gcg cat cct ctt ggg gct ctg			581
Met Ala Val Ala Ala Arg Glu Gly Asp Ala His Pro Leu Gly Ala Leu			
175	180	185	
cct gtg ggg acc ctc atc aac aac gtg gaa agt gag cca ggc cgg ggt			629
Pro Val Gly Thr Leu Ile Asn Asn Val Glu Ser Glu Pro Gly Arg Gly			
190	195	200	
gcc caa tat atc cga gct gca ggt gct gga aac gtg cgt agc aac agt			677
Ala Gln Tyr Ile Arg Ala Ala Gly Ala Gly Asn Val Arg Ser Asn Ser			
205	210	215	
agg ccg agt atc caa cgt tga tcataacaaa cgggtcattg gcaaggcagg			728
Arg Pro Ser Ile Gln Arg			
220	225		
tcgcaaccgc tggctgggca agaggcctaa cagtgggcgg tggcaccgca aggggggctg			788
ggctggccga aagattcggc cactaccccc catgaagagt tacgtgaagc tgccttctgc			848
ttctgcccga agctgatatc cctgtactct aataaaatgc ccccccccc cgttttaatc			908
tg			910

<210> 64  
 <211> 225  
 <212> PRT  
 <213> Homo sapiens

<400> 64  
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 Pro Pro Thr Val Ala Ala Pro Ala Pro Ser Leu Phe Pro Ala Ala Gln  
 20 25 30  
 Met Met Asn Asn Gly Leu Leu Gln Gln Pro Ser Ala Leu Met Leu Leu  
 35 40 45  
 Pro Cys Arg Pro Val Leu Thr Ser Val Ala Leu Asn Ala Asn Phe Val  
 50 55 60

Ser Trp Lys Ser Arg Thr Lys Tyr Thr Ile Thr Pro Val Lys Met Arg  
65 70 75 80  
Lys Ser Gly Gly Arg Asp His Thr Gly Arg Ile Arg Val His Gly Ile  
85 90 95  
Gly Gly Gly His Lys Gln Arg Tyr Arg Met Ile Asp Phe Leu Arg Phe  
100 105 110  
Arg Pro Glu Glu Thr Lys Ser Gly Pro Phe Glu Glu Lys Val Ile Gln  
115 120 125  
Val Arg Tyr Asp Pro Cys Arg Ser Ala Asp Ile Ala Leu Val Ala Gly  
130 135 140  
Gly Ser Arg Lys Arg Trp Ile Ile Ala Thr Glu Asn Met Gln Ala Gly  
145 150 155 160  
Asp Thr Ile Leu Asn Ser Asn His Ile Gly Arg Met Ala Val Ala Ala  
165 170 175  
Arg Glu Gly Asp Ala His Pro Leu Gly Ala Leu Pro Val Gly Thr Leu  
180 185 190  
Ile Asn Asn Val Glu Ser Glu Pro Gly Arg Gly Ala Gln Tyr Ile Arg  
195 200 205  
Ala Ala Gly Ala Gly Asn Val Arg Ser Asn Ser Arg Pro Ser Ile Gln  
210 215 220  
Arg  
225

<210> 65  
<211> 784  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (156)..(500)

<400> 65  
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ccgtggccta gcgccccgt ccccgccacc cgtgatcgtg cgccgaggcc cgcgaggggt 120  
cgccgcccag atcccaccag ccagcaagct aaagc atg gcg gcc atc ccc tcc 173  
Met Ala Ala Ile Pro Ser  
1 5  
agc ggc tcg ctc gtg gcc acc cac gac tac tac cgg cgc cgc ctg ggt 221  
Ser Gly Ser Leu Val Ala Thr His Asp Tyr Tyr Arg Arg Arg Leu Gly  
10 15 20  
tcc act tcc agc aac agc tcc tgc agc agt acc gag tgc ccc ggg gaa 269  
Ser Thr Ser Ser Asn Ser Ser Cys Ser Ser Thr Glu Cys Pro Gly Glu  
25 30 35  
gcc att ccc cac ccc cca ggt ctc ccc aag gct gac ccg ggt cat tgg 317  
Ala Ile Pro His Pro Pro Gly Leu Pro Lys Ala Asp Pro Gly His Trp  
40 45 50  
tgg gcc agc ttc ttt ttc ggg aag tcc acc ctc ccg ttc atg gcc acg 365  
Trp Ala Ser Phe Phe Phe Gly Lys Ser Thr Leu Pro Phe Met Ala Thr

098906888-092701

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55          60          65          70
gtg ttg gag tcc gca gag cac tcg gaa cct ccc cag gcc tcc agc agc 413
Val Leu Glu Ser Ala Glu His Ser Glu Pro Pro Gln Ala Ser Ser Ser
          75          80          85

atg acc gcc tgt ggc ctg gct cgg gac gcc ccg agg aag cag ccc ggc 461
Met Thr Ala Cys Gly Leu Ala Arg Asp Ala Pro Arg Lys Gln Pro Gly
          90          95          100

ggt cag tcc agc aca gcc agc gct ggg ccc ccg tcc tga cctgagcgg 510
Gly Gln Ser Ser Thr Ala Ser Ala Gly Pro Pro Ser
          105          110

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taccaccagc cccaggcctg cggaggcgct agtccaccag agccccctccc cgccccctctc 570

cccaactcgc atccctcgcc cccctcccca cctcccaccc cccaccctgt aaactaggcg 630

gctgcagcaa gcagaccttc gcatcaacac agcagacacc aaaaaccagt gagagccccg 690

ctctctaccg cccggcccca gcaactcgta gctttcctga cacctggaac tgtgcacctg 750

gcaccaagcg gaaaataaac tccaagcagc cagt 784

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<210> 66
<211> 114
<212> PRT
<213> Homo sapiens

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<400> 66
Met Ala Ala Ile Pro Ser Ser Gly Ser Leu Val Ala Thr His Asp Tyr
1          5          10          15
Tyr Arg Arg Arg Leu Gly Ser Thr Ser Ser Asn Ser Ser Cys Ser Ser
          20          25          30
Thr Glu Cys Pro Gly Glu Ala Ile Pro His Pro Pro Gly Leu Pro Lys
          35          40          45
Ala Asp Pro Gly His Trp Trp Ala Ser Phe Phe Phe Gly Lys Ser Thr
          50          55          60
Leu Pro Phe Met Ala Thr Val Leu Glu Ser Ala Glu His Ser Glu Pro
65          70          75          80
Pro Gln Ala Ser Ser Ser Met Thr Ala Cys Gly Leu Ala Arg Asp Ala
          85          90          95
Pro Arg Lys Gln Pro Gly Gly Gln Ser Ser Thr Ala Ser Ala Gly Pro
          100          105          110
Pro Ser

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<210> 67
<211> 984
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (348)..(770)

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<400> 67  
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aacagcgcgga gctgaggctg gggcccttgg cgcggaggct gagggaccog ccgcggcgct 120  
gtcgccggag agggagggca ccgctgtcgc cagaagccaa ggagtcctca gtgaccgtgg 180  
gatccacaac atctccacat cgctgtcccc acccagccag ggcagcgcca gcactagctc 240  
agacgcaagg acggaaccgc tggactccag gttccttgcc tgggagtagg agaaatccac 300  
ctgctggggg ctgagtgtgg cctgaggggac aggccctggg tcccggg atg ccc ctg 356  
Met Pro Leu  
1  
ccc gag ccc agc gag cag gag ggt gag agt gtg aag gcc agc cag gag 404  
Pro Glu Pro Ser Glu Gln Glu Gly Glu Ser Val Lys Ala Ser Gln Glu  
5 10 15  
cca tcc ccc aag cca ggc aca gaa gtc atc ccg gca gcc ccc agg aag 452  
Pro Ser Pro Lys Pro Gly Thr Glu Val Ile Pro Ala Ala Pro Arg Lys  
20 25 30 35  
ccc aga aag ttc tcc aaa ctg gtc ctg ctc aca gcc tcc aaa gac agc 500  
Pro Arg Lys Phe Ser Lys Leu Val Leu Thr Ala Ser Lys Asp Ser  
40 45 50  
acc aag gtg gcg ggg gcc aag cgc aag ggt gtg cac tgt gtc atg tcc 548  
Thr Lys Val Ala Gly Ala Lys Arg Lys Gly Val His Cys Val Met Ser  
55 60 65  
ctg ggg gtg ccc ggc ccc gcc acc ctt gcc aag gcc ctc ctc cag acc 596  
Leu Gly Val Pro Gly Pro Ala Thr Leu Ala Lys Ala Leu Leu Gln Thr  
70 75 80  
cac ccc gag gcc cag cgg gcc att gag gca gcc cct cag gag cct gag 644  
His Pro Glu Ala Gln Arg Ala Ile Glu Ala Ala Pro Gln Glu Pro Glu  
85 90 95  
cag aaa cgg agc agg cag gac cca ggc aca gac aga aca gaa gac agt 692  
Gln Lys Arg Ser Arg Gln Asp Pro Gly Thr Asp Arg Thr Glu Asp Ser  
100 105 110 115  
gga tta gca gcg ggg cct cct gag gct gct ggg gag aac ttt gcc ccc 740  
Gly Leu Ala Ala Gly Pro Pro Glu Ala Ala Gly Glu Asn Phe Ala Pro  
120 125 130  
tgc tct gtg gcg ccc ggc aag tcc ctg taa ccttgacaac aggcgcaccc 790  
Cys Ser Val Ala Pro Gly Lys Ser Leu  
135 140  
tcccggggcca ccaaccacgc cataggctct tctctgtccg cagggcttct ggggccaaat 850  
gggtgaatct ttgctttcaa cattgtgtga tttcttttct tttttttttt ttttttttag 910  
atcaagtata agttactttt gtaagcagaa aaatactttc aaacaagaat aaaagaagct 970

gttcgctaga cccc

984

<210> 68  
<211> 140  
<212> PRT  
<213> Homo sapiens

<400> 68  
Met Pro Leu Pro Glu Pro Ser Glu Gln Glu Gly Glu Ser Val Lys Ala  
1 5 10 15  
Ser Gln Glu Pro Ser Pro Lys Pro Gly Thr Glu Val Ile Pro Ala Ala  
20 25 30  
Pro Arg Lys Pro Arg Lys Phe Ser Lys Leu Val Leu Leu Thr Ala Ser  
35 40 45  
Lys Asp Ser Thr Lys Val Ala Gly Ala Lys Arg Lys Gly Val His Cys  
50 55 60  
Val Met Ser Leu Gly Val Pro Gly Pro Ala Thr Leu Ala Lys Ala Leu  
65 70 75 80  
Leu Gln Thr His Pro Glu Ala Gln Arg Ala Ile Glu Ala Ala Pro Gln  
85 90 95  
Glu Pro Glu Gln Lys Arg Ser Arg Gln Asp Pro Gly Thr Asp Arg Thr  
100 105 110  
Glu Asp Ser Gly Leu Ala Ala Gly Pro Pro Glu Ala Ala Gly Glu Asn  
115 120 125  
Phe Ala Pro Cys Ser Val Ala Pro Gly Lys Ser Leu  
130 135 140

<210> 69  
<211> 864  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (357)..(614)

<400> 69  
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cctccaggaa aagctcgcg aagacgaggt tctgcggaga gagaggctcc aagcagtctg 120  
ggaagtgtag tccagttggc ttagcagtag tttcgttggg ggggagccga ggttccggga 180  
aggggctagg ccggcttgaa aagagattat gactgtacct tttaactttg tagctggaac 240  
acaagaagtg tttgtttaat gaatgacgta cacatttaag atctgtttgg acgcggagga 300  
taatcctgtg aattgctaata agttcactgg gtttggccct tagtggttgac ttcagt atg 359  
Met  
1

ctg aga cgg aaa cca aca cgc cta gag cta aag ctt gat gac att gaa 407  
Leu Arg Arg Lys Pro Thr Arg Leu Glu Leu Lys Leu Asp Asp Ile Glu

	5	10	15	
gag ttt gag aac att cga aag gac ctg gag acc cgt aag aaa cag aag				455
Glu Phe Glu Asn Ile Arg Lys Asp Leu Glu Thr Arg Lys Lys Gln Lys				
	20	25	30	
gaa gat gtg gaa gtt gta gga ggc agt gat gga gaa gga gcc att ggg				503
Glu Asp Val Glu Val Val Gly Gly Ser Asp Gly Glu Gly Ala Ile Gly				
	35	40	45	
ctt agc agt gat ccc aag agc cgg gaa caa atg atc aat gat cgg att				551
Leu Ser Ser Asp Pro Lys Ser Arg Glu Gln Met Ile Asn Asp Arg Ile				
	50	55	60	65
ggg tat aaa ccc caa ccc aag ccc aat aat cgt tca tct caa ttt gga				599
Gly Tyr Lys Pro Gln Pro Lys Pro Asn Asn Arg Ser Ser Gln Phe Gly				
	70	75	80	
agt ctt gaa ttt tag agatggatta tcttgcatgc cagagcgctg gaatggaata				654
Ser Leu Glu Phe				
	85			
aaatgatggc agaagtacaa accagattta gagaattgag tgcttgccagt caagcagaat				714
gtacctcctg cagagacaaa tcttctgcat gagattactg atgcttcaact tgcactctaa				774
gctggaatcc aaactctggt ttgtctcttg aaaatttgac tctataaaac tgatctgatt				834
ttctgttttt aaaaataaat atatttttgg				864

<210> 70  
 <211> 85  
 <212> PRT  
 <213> Homo sapiens

<400> 70  
 Met Leu Arg Arg Lys Pro Thr Arg Leu Glu Leu Lys Leu Asp Asp Ile  
 1 5 10 15  
 Glu Glu Phe Glu Asn Ile Arg Lys Asp Leu Glu Thr Arg Lys Lys Gln  
 20 25 30  
 Lys Glu Asp Val Glu Val Val Gly Gly Ser Asp Gly Glu Gly Ala Ile  
 35 40 45  
 Gly Leu Ser Ser Asp Pro Lys Ser Arg Glu Gln Met Ile Asn Asp Arg  
 50 55 60  
 Ile Gly Tyr Lys Pro Gln Pro Lys Pro Asn Asn Arg Ser Ser Gln Phe  
 65 70 75 80  
 Gly Ser Leu Glu Phe  
 85

<210> 71  
 <211> 2617  
 <212> DNA  
 <213> Homo sapiens

<220>

<221> CDS

<222> (121)..(1860)

<400> 71

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tcgccccgct agtcctgcct gtctcccggt gcagctgtgt tcgcggcctg caggcccaac 120

atg gcg cag gag gtg tcg gag tac ctg agc cag aac ccg cgg gtg gca 168  
Met Ala Gln Glu Val Ser Glu Tyr Leu Ser Gln Asn Pro Arg Val Ala  
1 5 10 15

gcc tgg gtg gag gcg ctg cgc tgc gac ggc gag act gac aaa cac tgg 216  
Ala Trp Val Glu Ala Leu Arg Cys Asp Gly Glu Thr Asp Lys His Trp  
20 25 30

cgc cac cgc cgg gat ttt ttg ctt cgc aac gcc ggg gac ctg gcc ccc 264  
Arg His Arg Arg Asp Phe Leu Leu Arg Asn Ala Gly Asp Leu Ala Pro  
35 40 45

gct ggc ggc gct gcc tcc gct agc acg gat gaa gct gcc gac gcc gag 312  
Ala Gly Gly Ala Ala Ser Ala Ser Thr Asp Glu Ala Ala Asp Ala Glu  
50 55 60

agc ggg acc cga aac cgg cag ctg cag cag ctc atc tcc ttt tcc atg 360  
Ser Gly Thr Arg Asn Arg Gln Leu Gln Gln Leu Ile Ser Phe Ser Met  
65 70 75 80

gcc tgg gcg aac cac gtc ttc ctc ggg tgc cga tac cct caa aaa gtt 408  
Ala Trp Ala Asn His Val Phe Leu Gly Cys Arg Tyr Pro Gln Lys Val  
85 90 95

atg gat aaa ata ctt agt atg gct gaa ggc atc aaa gtg aca gat gct 456  
Met Asp Lys Ile Leu Ser Met Ala Glu Gly Ile Lys Val Thr Asp Ala  
100 105 110

cca acc tat aca aca aga gat gaa ctg gtt gcc aag gtg aag aaa aga 504  
Pro Thr Tyr Thr Thr Arg Asp Glu Leu Val Ala Lys Val Lys Lys Arg  
115 120 125

ggg ata tcg agt agc aat gaa ggg gta gaa gag cca tcc aaa aaa cga 552  
Gly Ile Ser Ser Ser Asn Glu Gly Val Glu Glu Pro Ser Lys Lys Arg  
130 135 140

gtt ata gaa gga aaa aac agt tct gca gtt gag caa gat cac gca aaa 600  
Val Ile Glu Gly Lys Asn Ser Ser Ala Val Glu Gln Asp His Ala Lys  
145 150 155 160

acc tct gcc aag aca gaa cgt gca tca gct cag cag gaa aac agt tca 648  
Thr Ser Ala Lys Thr Glu Arg Ala Ser Ala Gln Gln Glu Asn Ser Ser  
165 170 175

acg tgt ata ggg tcg gcc atc aaa tca gag agt ggg aac tca gct cgg 696  
Thr Cys Ile Gly Ser Ala Ile Lys Ser Glu Ser Gly Asn Ser Ala Arg  
180 185 190



agc tct ggc atc tcc agt cag aat agc tct aca agt gat gga gat cga	744
Ser Ser Gly Ile Ser Ser Gln Asn Ser Ser Thr Ser Asp Gly Asp Arg	
195 200 205	
tct gtt tcc agc caa agc agc agc agc gtt tcc tct cag gta aca acg	792
Ser Val Ser Ser Gln Ser Ser Ser Ser Val Ser Ser Gln Val Thr Thr	
210 215 220	
gca gga tct ggg aaa gct tct gaa gca gaa gct cca gat aaa cac ggt	840
Ala Gly Ser Gly Lys Ala Ser Glu Ala Glu Ala Pro Asp Lys His Gly	
225 230 235 240	
tca tca ttt gtt tcc ttg ctg aaa tcc agt gtg aat agt cac atg acc	888
Ser Ser Phe Val Ser Leu Leu Lys Ser Ser Val Asn Ser His Met Thr	
245 250 255	
caa tcc act gat tct aga caa caa agt gga tca cct aaa aag agt gct	936
Gln Ser Thr Asp Ser Arg Gln Gln Ser Gly Ser Pro Lys Lys Ser Ala	
260 265 270	
ttg gaa ggc tct tca gcc tca gct tct cga agc agc tca gag atc gag	984
Leu Glu Gly Ser Ser Ala Ser Ala Ser Arg Ser Ser Ser Glu Ile Glu	
275 280 285	
gtg ccc ttg ttg ggc tcc tca gga agc tca gag gta gaa ttg cca cta	1032
Val Pro Leu Leu Gly Ser Ser Gly Ser Ser Glu Val Glu Leu Pro Leu	
290 295 300	
ttg tct tcc aaa cct agt tca gag aca gct tca agt ggg tta act tcc	1080
Leu Ser Ser Lys Pro Ser Ser Glu Thr Ala Ser Ser Gly Leu Thr Ser	
305 310 315 320	
aaa act agt tca gag gca agt gtt tca tca tca gtt gct aaa aac agt	1128
Lys Thr Ser Ser Glu Ala Ser Val Ser Ser Ser Val Ala Lys Asn Ser	
325 330 335	
tcc tca tca ggc aca tcc tta ctg act ccc aag agc agc tct tca aca	1176
Ser Ser Ser Gly Thr Ser Leu Leu Thr Pro Lys Ser Ser Ser Ser Thr	
340 345 350	
aat aca tcg ctg cta act tcc aag agc act tcc cag gta gct gca tca	1224
Asn Thr Ser Leu Leu Thr Ser Lys Ser Thr Ser Gln Val Ala Ala Ser	
355 360 365	
cta cta gct tcc aag agc agc tcc cag acc agt gga tct ctg gtt tcc	1272
Leu Leu Ala Ser Lys Ser Ser Ser Gln Thr Ser Gly Ser Leu Val Ser	
370 375 380	
aaa agc act tcc tta gca agt gtg tcc cag ttg gct tct aag agt agt	1320
Lys Ser Thr Ser Leu Ala Ser Val Ser Gln Leu Ala Ser Lys Ser Ser	
385 390 395 400	
tct cag act agc acc tca cag ttg cct tct aaa agt act tca cag tca	1368
Ser Gln Thr Ser Thr Ser Gln Leu Pro Ser Lys Ser Thr Ser Gln Ser	
405 410 415	
agt gag agt tct gtc aaa ttc tct tgc aag tta acc aat gaa gat gtg	1416

Ser	Glu	Ser	Ser	Val	Lys	Phe	Ser	Cys	Lys	Leu	Thr	Asn	Glu	Asp	Val		
			420				425						430				
aaa	cag	aag	caa	cct	ttt	ttc	aat	aga	cta	tat	aaa	acg	gtg	gca	tgg	1464	
Lys	Gln	Lys	Gln	Pro	Phe	Phe	Asn	Arg	Leu	Tyr	Lys	Thr	Val	Ala	Trp		
			435				440						445				
aag	ttg	gta	gct	gtt	ggg	ggc	ttt	agt	ccc	aat	gtg	aat	cat	gga	gag	1512	
Lys	Leu	Val	Ala	Val	Gly	Gly	Phe	Ser	Pro	Asn	Val	Asn	His	Gly	Glu		
			450				455						460				
ctc	cta	aat	gca	gct	att	gag	gct	ctg	aaa	gca	aca	ctg	gat	gta	ttt	1560	
Leu	Leu	Asn	Ala	Ala	Ile	Glu	Ala	Leu	Lys	Ala	Thr	Leu	Asp	Val	Phe		
			465				470						475			480	
ttt	gtc	cca	cta	aaa	gaa	ttg	gca	gat	ctg	cct	caa	aat	aag	agc	tct	1608	
Phe	Val	Pro	Leu	Lys	Glu	Leu	Ala	Asp	Leu	Pro	Gln	Asn	Lys	Ser	Ser		
			485				490						495				
caa	gaa	agt	att	gtt	tgt	gaa	ttg	agg	tgc	aag	tct	gtg	tat	ttg	ggc	1656	
Gln	Glu	Ser	Ile	Val	Cys	Glu	Leu	Arg	Cys	Lys	Ser	Val	Tyr	Leu	Gly		
			500				505						510				
act	ggc	tgt	gga	aaa	agc	aaa	gaa	aat	gca	aaa	gca	gtt	gca	tca	aga	1704	
Thr	Gly	Cys	Gly	Lys	Ser	Lys	Glu	Asn	Ala	Lys	Ala	Val	Ala	Ser	Arg		
			515				520						525				
gaa	gca	ttg	aag	tta	ttt	ctc	aag	aaa	aag	gtg	gtg	gta	aaa	ata	tgt	1752	
Glu	Ala	Leu	Lys	Leu	Phe	Leu	Lys	Lys	Lys	Val	Val	Val	Lys	Ile	Cys		
			530				535						540				
aaa	agg	aaa	tac	aga	ggc	agt	gaa	ata	gaa	gat	cta	gta	ctc	ctt	gat	1800	
Lys	Arg	Lys	Tyr	Arg	Gly	Ser	Glu	Ile	Glu	Asp	Leu	Val	Leu	Leu	Asp		
			545				550						555			560	
gaa	gaa	tcg	agg	cct	gta	aac	tta	cct	cca	gca	cta	aaa	cat	cct	caa	1848	
Glu	Glu	Ser	Arg	Pro	Val	Asn	Leu	Pro	Pro	Ala	Leu	Lys	His	Pro	Gln		
			565				570						575				
gaa	tta	cta	taa	tgtgtccaaa	atatcactgc	atacaatatc	tggtatttga									1900	
Glu	Leu	Leu															
agagaaaaac tgacttttgt atagtataaa acacaggctt tcacaaattt tgtatttgctt 1960																	
tttttccagt tttgcagaaa atttacattc tagttctctt cacacagtag cagttgtaaa 2020																	
taatttatga atgacagtac acattaaaag gtatgcatta gcagcatatt agtatgtgt 2080																	
tttatttgct gaagaaaata ctgtcttcta tttttaatga tacattaggt acgatgtgta 2140																	
gttcggtaga gtctaaaaat ttttgtacta ctttcaattt ggtgaaaatg tattaagttg 2200																	
tctaccatgt tttcttttct agctgaataa accacatcaa aggaaaggga ccacagtatt 2260																	
tgaatgtttg aaagtctgta aagcttaagg ttttaaaaat gttgcccgta atgttgaacg 2320																	
tgtctgttaa aaaataaaaag aaaaaataagt tgcttcaaac tatttttatg agaagttgta 2380																	

agcatttttt agatataaag cagtataaag tacttggtat tttactctga agttgtttaa 2440  
aattccacat gactttgacc gctgaagatt ctttaagcgg gttaatttat gttttgaggt 2500  
ggaatacaat ttacactttt ttcttaaaaa catgaatgtg ggtttctata ttaagcatat 2560  
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<210> 72  
<211> 579  
<212> PRT  
<213> Homo sapiens

<400> 72  
Met Ala Gln Glu Val Ser Glu Tyr Leu Ser Gln Asn Pro Arg Val Ala  
1 5 10 15  
Ala Trp Val Glu Ala Leu Arg Cys Asp Gly Glu Thr Asp Lys His Trp  
20 25 30  
Arg His Arg Arg Asp Phe Leu Leu Arg Asn Ala Gly Asp Leu Ala Pro  
35 40 45  
Ala Gly Gly Ala Ala Ser Ala Ser Thr Asp Glu Ala Ala Asp Ala Glu  
50 55 60  
Ser Gly Thr Arg Asn Arg Gln Leu Gln Gln Leu Ile Ser Phe Ser Met  
65 70 75 80  
Ala Trp Ala Asn His Val Phe Leu Gly Cys Arg Tyr Pro Gln Lys Val  
85 90 95  
Met Asp Lys Ile Leu Ser Met Ala Glu Gly Ile Lys Val Thr Asp Ala  
100 105 110  
Pro Thr Tyr Thr Thr Arg Asp Glu Leu Val Ala Lys Val Lys Lys Arg  
115 120 125  
Gly Ile Ser Ser Ser Asn Glu Gly Val Glu Glu Pro Ser Lys Lys Arg  
130 135 140  
Val Ile Glu Gly Lys Asn Ser Ser Ala Val Glu Gln Asp His Ala Lys  
145 150 155 160  
Thr Ser Ala Lys Thr Glu Arg Ala Ser Ala Gln Gln Glu Asn Ser Ser  
165 170 175  
Thr Cys Ile Gly Ser Ala Ile Lys Ser Glu Ser Gly Asn Ser Ala Arg  
180 185 190  
Ser Ser Gly Ile Ser Ser Gln Asn Ser Ser Thr Ser Asp Gly Asp Arg  
195 200 205  
Ser Val Ser Ser Gln Ser Ser Ser Val Ser Ser Gln Val Thr Thr  
210 215 220  
Ala Gly Ser Gly Lys Ala Ser Glu Ala Glu Ala Pro Asp Lys His Gly  
225 230 235 240  
Ser Ser Phe Val Ser Leu Leu Lys Ser Ser Val Asn Ser His Met Thr  
245 250 255  
Gln Ser Thr Asp Ser Arg Gln Gln Ser Gly Ser Pro Lys Lys Ser Ala  
260 265 270  
Leu Glu Gly Ser Ser Ala Ser Ala Ser Arg Ser Ser Ser Glu Ile Glu  
275 280 285  
Val Pro Leu Leu Gly Ser Ser Gly Ser Ser Glu Val Glu Leu Pro Leu  
290 295 300  
Leu Ser Ser Lys Pro Ser Ser Glu Thr Ala Ser Ser Gly Leu Thr Ser  
305 310 315 320  
Lys Thr Ser Ser Glu Ala Ser Val Ser Ser Ser Val Ala Lys Asn Ser

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				325					330					335	
Ser	Ser	Ser	Gly	Thr	Ser	Leu	Leu	Thr	Pro	Lys	Ser	Ser	Ser	Ser	Thr
			340					345					350		
Asn	Thr	Ser	Leu	Leu	Thr	Ser	Lys	Ser	Thr	Ser	Gln	Val	Ala	Ala	Ser
		355					360					365			
Leu	Leu	Ala	Ser	Lys	Ser	Ser	Ser	Gln	Thr	Ser	Gly	Ser	Leu	Val	Ser
	370					375					380				
Lys	Ser	Thr	Ser	Leu	Ala	Ser	Val	Ser	Gln	Leu	Ala	Ser	Lys	Ser	Ser
385					390					395					400
Ser	Gln	Thr	Ser	Thr	Ser	Gln	Leu	Pro	Ser	Lys	Ser	Thr	Ser	Gln	Ser
				405					410					415	
Ser	Glu	Ser	Ser	Val	Lys	Phe	Ser	Cys	Lys	Leu	Thr	Asn	Glu	Asp	Val
			420					425					430		
Lys	Gln	Lys	Gln	Pro	Phe	Phe	Asn	Arg	Leu	Tyr	Lys	Thr	Val	Ala	Trp
		435					440					445			
Lys	Leu	Val	Ala	Val	Gly	Gly	Phe	Ser	Pro	Asn	Val	Asn	His	Gly	Glu
	450					455					460				
Leu	Leu	Asn	Ala	Ala	Ile	Glu	Ala	Leu	Lys	Ala	Thr	Leu	Asp	Val	Phe
465					470					475					480
Phe	Val	Pro	Leu	Lys	Glu	Leu	Ala	Asp	Leu	Pro	Gln	Asn	Lys	Ser	Ser
				485					490					495	
Gln	Glu	Ser	Ile	Val	Cys	Glu	Leu	Arg	Cys	Lys	Ser	Val	Tyr	Leu	Gly
			500					505					510		
Thr	Gly	Cys	Gly	Lys	Ser	Lys	Glu	Asn	Ala	Lys	Ala	Val	Ala	Ser	Arg
		515					520					525			
Glu	Ala	Leu	Lys	Leu	Phe	Leu	Lys	Lys	Lys	Val	Val	Val	Lys	Ile	Cys
	530					535					540				
Lys	Arg	Lys	Tyr	Arg	Gly	Ser	Glu	Ile	Glu	Asp	Leu	Val	Leu	Leu	Asp
545					550					555					560
Glu	Glu	Ser	Arg	Pro	Val	Asn	Leu	Pro	Pro	Ala	Leu	Lys	His	Pro	Gln
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Glu	Leu	Leu													

<210> 73  
 <211> 1810  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (39)..(1121)

<400> 73  
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 Met Asp Thr Pro Leu Arg  
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cgc agc cga cgg ctg gga ggc cta agg ccc gaa tcc ccc gag agc ctc 104  
 Arg Ser Arg Arg Leu Gly Gly Leu Arg Pro Glu Ser Pro Glu Ser Leu  
 10 15 20

acc tca gtt tcg cgg acg aga cgg gcc ctt gtg gag ttc gag tcg aac 152  
 Thr Ser Val Ser Arg Thr Arg Arg Ala Leu Val Glu Phe Glu Ser Asn  
 25 30 35

cca gaa gaa acg agg gag ccc ggg tct cct ccg agt gtg cag cgg gct	200
Pro Glu Glu Thr Arg Glu Pro Gly Ser Pro Pro Ser Val Gln Arg Ala	
40 45 50	
ggc ctg ggg tcc ccc gaa agg ccg ccg aag aca agc cca gga tca ccc	248
Gly Leu Gly Ser Pro Glu Arg Pro Pro Lys Thr Ser Pro Gly Ser Pro	
55 60 65 70	
cgt ctg cag cag ggt gca ggc ttg gag tca ccc caa ggg cag cca gag	296
Arg Leu Gln Gln Gly Ala Gly Leu Glu Ser Pro Gln Gly Gln Pro Glu	
75 80 85	
cca ggc gca gcg tcc ccc cag cgt cag caa gac cta cac ctg gag tcg	344
Pro Gly Ala Ala Ser Pro Gln Arg Gln Gln Asp Leu His Leu Glu Ser	
90 95 100	
cct caa aga cag cca gag tac agt cct gaa tcc cca cga tgt cag ccg	392
Pro Gln Arg Gln Pro Glu Tyr Ser Pro Glu Ser Pro Arg Cys Gln Pro	
105 110 115	
aag cca agt gag gag gca cca aag tgt tct cag gac cag gga gta ctg	440
Lys Pro Ser Glu Glu Ala Pro Lys Cys Ser Gln Asp Gln Gly Val Leu	
120 125 130	
gcc tcg gag ttg gcc cag aat aag gag gag ctg acc ccg ggg gcc ccc	488
Ala Ser Glu Leu Ala Gln Asn Lys Glu Glu Leu Thr Pro Gly Ala Pro	
135 140 145 150	
cag cat cag cta ccg ccg gtc cca gga tca cca gag cct tac ccc ggt	536
Gln His Gln Leu Pro Pro Val Pro Gly Ser Pro Glu Pro Tyr Pro Gly	
155 160 165	
cag caa gct ccc ggt ccg gag ccc tct cag cca cta ctg gag ctg aca	584
Gln Gln Ala Pro Gly Pro Glu Pro Ser Gln Pro Leu Leu Glu Leu Thr	
170 175 180	
ccc agg gca cct ggc tcc ccc ccg ggt cag cat gag ccg agc aag cca	632
Pro Arg Ala Pro Gly Ser Pro Arg Gly Gln His Glu Pro Ser Lys Pro	
185 190 195	
cct cca gct ggg gag acg gtg aca ggc ggc ttc ggg gca aag aag cga	680
Pro Pro Ala Gly Glu Thr Val Thr Gly Gly Phe Gly Ala Lys Lys Arg	
200 205 210	
aaa ggt tct tca tcc cag gcc cca gcg tcc aag aag ttg aat aaa gag	728
Lys Gly Ser Ser Ser Gln Ala Pro Ala Ser Lys Lys Leu Asn Lys Glu	
215 220 225 230	
gag ctt cct gta atc ccg aag ggg aag ccc aaa tcg ggg cga gtg tgg	776
Glu Leu Pro Val Ile Pro Lys Gly Lys Pro Lys Ser Gly Arg Val Trp	
235 240 245	
aag gac cgc tcc aag aaa aga ttc tcc cag atg ctt cag gac aag ccc	824
Lys Asp Arg Ser Lys Lys Arg Phe Ser Gln Met Leu Gln Asp Lys Pro	
250 255 260	
ctg cgc aca tcg tgg cag ccg aag atg aag gaa cga cag gag agg aag	872

Leu Arg Thr Ser Trp Gln Arg Lys Met Lys Glu Arg Gln Glu Arg Lys  
 265 270 275  
 ctg gcc aag gac ttt gcc cgt cac ctg gag gag gag aag gag agg cgc 920  
 Leu Ala Lys Asp Phe Ala Arg His Leu Glu Glu Glu Lys Glu Arg Arg  
 280 285 290  
 cgc cag gag aag aaa cag cgc cgg gct gag aac ctg aaa cgc cgc ctg 968  
 Arg Gln Glu Lys Lys Gln Arg Arg Ala Glu Asn Leu Lys Arg Arg Leu  
 295 300 305 310  
 gag aat gag cgg aag gca gag gtc gtc caa gtg atc cga aac ccc gcc 1016  
 Glu Asn Glu Arg Lys Ala Glu Val Val Gln Val Ile Arg Asn Pro Ala  
 315 320 325  
 aag ctc aag cgg gca aag aag aag cag ctg cgc tcc att gag aag cgg 1064  
 Lys Leu Lys Arg Ala Lys Lys Lys Gln Leu Arg Ser Ile Glu Lys Arg  
 330 335 340  
 gac acc ctg gcc ctg ctg cag aag cag ccg ccc cag cag ccg gca gcc 1112  
 Asp Thr Leu Ala Leu Leu Gln Lys Gln Pro Pro Gln Gln Pro Ala Ala  
 345 350 355  
 aag atc tga gctcaggacg gcccagggcc ttccatggcc aacaaccatg 1161  
 Lys Ile  
 360  
 tcagacacag cacctcaggc cgctgctcag atgcctctgc tggagctggc actccaaacc 1221  
 catggctcca gaacagggac cccacccccg accggggctc ctcagccttt gaaggcttcc 1281  
 aggcaggtct gtgtgggaca gaagccaaaa gggtcctggg acctggcaga gatgggggag 1341  
 ggaagagatt cagctcccat cctccttcc tctccttctc caagtgcctt caaaccaaga 1401  
 actgtacatt cttctgggtc ctcagtgcgc tgggtgactg caggtgactc cctcagcagt 1461  
 gtatgccctt tctcagcatc ctaggtccat cccaggcctg gaggtgaca gttgggaatc 1521  
 cagcttcccc cacaccttcc caaaggctgc tctgagcacc tccacacccc actgcctctg 1581  
 tccccagcaa actgaatccg gttcctctcc acttttcaat actgaaagat taaaatgggg 1641  
 aggttgacag gagcagagct tttccctagc acccactttc ccaaaccagt ctctgcagaa 1701  
 gccccagaga atctaactca tgctgtcca gtctacagca aaaatattta ttgagtgcct 1761  
 gttgcataca ggcacaatcc taggcactgg caaatacaga caatagacc 1810  
 <210> 74  
 <211> 360  
 <212> PRT  
 <213> Homo sapiens  
 <400> 74  
 Met Asp Thr Pro Leu Arg Arg Ser Arg Arg Leu Gly Gly Leu Arg Pro

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1		5		10		15
Glu	Ser	Pro	Glu	Ser	Leu	Thr
		20				
Val	Glu	Phe	Glu	Ser	Asn	Pro
		35			40	
Pro	Ser	Val	Gln	Arg	Ala	Gly
		50			55	
Thr	Ser	Pro	Gly	Ser	Pro	Arg
		65			70	
Pro	Gln	Gly	Gln	Pro	Glu	Pro
			85			
Asp	Leu	His	Leu	Glu	Ser	Pro
		100				
Ser	Pro	Arg	Cys	Gln	Pro	Lys
		115			120	
Gln	Asp	Gln	Gly	Val	Leu	Ala
		130			135	
Leu	Thr	Pro	Gly	Ala	Pro	Gln
		145			150	
Pro	Glu	Pro	Tyr	Pro	Gly	Gln
			165			
Pro	Leu	Leu	Glu	Leu	Thr	Pro
		180				
His	Glu	Pro	Ser	Lys	Pro	Pro
		195			200	
Phe	Gly	Ala	Lys	Lys	Arg	Lys
		210			215	
Lys	Lys	Leu	Asn	Lys	Glu	Glu
		225			230	
Lys	Ser	Gly	Arg	Val	Trp	Lys
			245			
Met	Leu	Gln	Asp	Lys	Pro	Leu
		260				
Glu	Arg	Gln	Glu	Arg	Lys	Leu
		275			280	
Glu	Glu	Lys	Glu	Arg	Arg	Arg
		290			295	
Asn	Leu	Lys	Arg	Arg	Leu	Glu
		305			310	
Val	Ile	Arg	Asn	Pro	Ala	Lys
			325			
Arg	Ser	Ile	Glu	Lys	Arg	Asp
		340				
Pro	Gln	Gln	Pro	Ala	Ala	Lys
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<210> 75  
 <211> 1620  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (217)..(597)

<400> 75

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ccccaccac cgcccttgcc gccatcgcca cctccgccgc tgccgccttg gggccctect 120  
ccttcaccgc ccccttcacc acctctacac gttctaggcc ttctgtcctg gagaagaagc 180  
tatagtcgtt ctcccttggt ggcccggggc gcagcc atg gcg gac ggc ggc ggc 234  
Met Ala Asp Gly Gly Gly  
1 5  
ggc ggc gga act ggc gcg gtg ggc ggc ggc gga act agc cag gcc tct 282  
Gly Gly Gly Thr Gly Ala Val Gly Gly Gly Gly Thr Ser Gln Ala Ser  
10 15 20  
gcc ggc gca gcg act ggc gct act ggc gcc agc ggc ggc ggt ggc ccc 330  
Ala Gly Ala Ala Thr Gly Ala Thr Gly Ala Ser Gly Gly Gly Gly Pro  
25 30 35  
atc aac ccg gcc tcg ctg cct ccc ggc gac ccg cag ctc atc gct ctc 378  
Ile Asn Pro Ala Ser Leu Pro Gly Asp Pro Gln Leu Ile Ala Leu  
40 45 50  
atc gtg gag cag ctc aag agc cgg ggc ctt ttt gac agc ttc cgc cgg 426  
Ile Val Glu Gln Leu Lys Ser Arg Gly Leu Phe Asp Ser Phe Arg Arg  
55 60 65 70  
gac tgc ctg gcc gac gtg gac acc aag cca gct tac caa aac ctg agg 474  
Asp Cys Leu Ala Asp Val Asp Thr Lys Pro Ala Tyr Gln Asn Leu Arg  
75 80 85  
cag aaa gtg gat aat ttt gtg tca aca cat ctg gac aag cag gaa tgg 522  
Gln Lys Val Asp Asn Phe Val Ser Thr His Leu Asp Lys Gln Glu Trp  
90 95 100  
aat cct acg atg aac aaa aac cag ttg cga aat ggt ctg agg cag agt 570  
Asn Pro Thr Met Asn Lys Asn Gln Leu Arg Asn Gly Leu Arg Gln Ser  
105 110 115  
gtg gtt cag ttg ggt gat tgt ggc tga gattgtgcag taggaataac 617  
Val Val Gln Leu Gly Asp Cys Gly  
120 125  
agctgctggt tgagaattac ccctcaaaag tgaaaatagc gtgagctgta tatggtcagg 677  
gatgttgga gctggagtag acaggattat ttctcaggtg gtggatcaa aacttaacca 737  
catcttcagg ccacaaatag aacgagcaat tcatgagttc ctggcggccc agaaaaaagc 797  
agctgtgcc gacccccctc cagagcccga aggccaggac cctccagctc catctcagga 857  
cacttcctaa gaatacgcca gacacctttt gaaagcta ttttggtgaa gaaatggatt 917  
cggttacata agagtgaac ttcagactga agataggcca aggtcgtcac tgatctcaag 977  
atttcaacct tgaccatggg cagtgaccag attgaaaggg gagcaagttc ggcagtggga 1037  
gagttgaccg tgtcaccccc tgcattgtgc tgccatttgg ccagcctgtc caagggcatg 1097



acaccaagta gacactacag agagagaaac actacagcaa cccaggggtg tcctgaaaca 1157  
gacttttata cttgaacatg gagactgcac atggacttta gggtttgtgc tgtgggataa 1217  
acggaagcta cagtgagaac atagccagtc ccaaagacaa tttcaaagaa aaatgacagt 1277  
aaagattagc tgggagtagt ctttgacagt gcttatttga tactgtctct cagagtttgc 1337  
aaaccagatt gtacaagtca ttagcgtcag atagctttaa agttgtgacc ttcttgtaca 1397  
tgaatcttct agccagtttc ctttcctttg taacgaaaca tgaaatccta gaatgtatga 1457  
gaagttcaga cattagcat aaggaaactc gtttgcaggc tctctgtcca gggctgcttc 1517  
ctgtcctgga ggggccagtg agtcttaggt atgtttattt tattctcaca tttgtgtttt 1577  
tttagaaaag tgaatgggtca ataaatggct tatctttcat aat 1620

<210> 76  
<211> 126  
<212> PRT  
<213> Homo sapiens

<400> 76  
Met Ala Asp Gly Gly Gly Gly Gly Gly Thr Gly Ala Val Gly Gly Gly  
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Gly Thr Ser Gln Ala Ser Ala Gly Ala Ala Thr Gly Ala Thr Gly Ala  
20 25 30  
Ser Gly Gly Gly Gly Pro Ile Asn Pro Ala Ser Leu Pro Pro Gly Asp  
35 40 45  
Pro Gln Leu Ile Ala Leu Ile Val Glu Gln Leu Lys Ser Arg Gly Leu  
50 55 60  
Phe Asp Ser Phe Arg Arg Asp Cys Leu Ala Asp Val Asp Thr Lys Pro  
65 70 75 80  
Ala Tyr Gln Asn Leu Arg Gln Lys Val Asp Asn Phe Val Ser Thr His  
85 90 95  
Leu Asp Lys Gln Glu Trp Asn Pro Thr Met Asn Lys Asn Gln Leu Arg  
100 105 110  
Asn Gly Leu Arg Gln Ser Val Val Gln Leu Gly Asp Cys Gly  
115 120 125

<210> 77  
<211> 1349  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (185)..(1042)

<400> 77  
gtatttccaa ggactccaaa gcgaggccgg ggactgaagg tgtgggtgtc gagccctctg 60

gcagaggggtt aacctgggtc aaatgcacgg attctcacct cgtacagtta cgctctcccg 120  
 cggcacgtcc gcgaggactt gaagtcctga gcgctcaagt ttgtccgtag gtcgagagaa 180  
 ggcc atg gag gtg ccg cca ccg gca ccg cgg agc ttt ctc tgt aga gca 229  
 Met Glu Val Pro Pro Pro Ala Pro Arg Ser Phe Leu Cys Arg Ala  
 1 5 10 15  
 ttg tgc cta ttt ccc cga gtc ttt gct gcc gaa gct gtg act gcc gat 277  
 Leu Cys Leu Phe Pro Arg Val Phe Ala Ala Glu Ala Val Thr Ala Asp  
 20 25 30  
 tcg gaa gtc ctt gag gag cgt cag aag cgg ctt ccc tac gtc cca gag 325  
 Ser Glu Val Leu Glu Glu Arg Gln Lys Arg Leu Pro Tyr Val Pro Glu  
 35 40 45  
 ccc tat tac ccg gaa tct gga tgg gac cgc ctc cgg gag ctg ttt ggc 373  
 Pro Tyr Tyr Pro Glu Ser Gly Trp Asp Arg Leu Arg Glu Leu Phe Gly  
 50 55 60  
 aaa gat gaa cag cag aga att tca aag gac ctt gct aat atc tgt aag 421  
 Lys Asp Glu Gln Gln Arg Ile Ser Lys Asp Leu Ala Asn Ile Cys Lys  
 65 70 75  
 acg gca gct aca gca ggc atc att ggc tgg gtg tat ggg gga ata cca 469  
 Thr Ala Ala Thr Ala Gly Ile Ile Gly Trp Val Tyr Gly Gly Ile Pro  
 80 85 90 95  
 gct ttt att cat gct aaa caa caa tac att gag cag agc cag gca gaa 517  
 Ala Phe Ile His Ala Lys Gln Gln Tyr Ile Glu Gln Ser Gln Ala Glu  
 100 105 110  
 att tat cat aac cgg ttt gat gct gtg caa tct gca cat cgt gct gcc 565  
 Ile Tyr His Asn Arg Phe Asp Ala Val Gln Ser Ala His Arg Ala Ala  
 115 120 125  
 aca cga ggc ttc att cgt tat ggc tgg cgc tgg ggt tgg aga act gca 613  
 Thr Arg Gly Phe Ile Arg Tyr Gly Trp Arg Trp Gly Trp Arg Thr Ala  
 130 135 140  
 gtg ttt gtg act ata ttc aac aca gtg aac act agt ctg aat gta tac 661  
 Val Phe Val Thr Ile Phe Asn Thr Val Asn Thr Ser Leu Asn Val Tyr  
 145 150 155  
 cga aat aaa gat gcc tta agc cat ttt gta att gca gga gct gtc acg 709  
 Arg Asn Lys Asp Ala Leu Ser His Phe Val Ile Ala Gly Ala Val Thr  
 160 165 170 175  
 gga agt ctt ttt agg ata aac gta ggc ctg cgt ggc ctg gtg gct ggt 757  
 Gly Ser Leu Phe Arg Ile Asn Val Gly Leu Arg Gly Leu Val Ala Gly  
 180 185 190  
 ggc ata att gga gcc ttg ctg ggc act cct gta gga ggc ctg ctg atg 805  
 Gly Ile Ile Gly Ala Leu Leu Gly Thr Pro Val Gly Gly Leu Leu Met  
 195 200 205  
 gca ttt cag aag tac tct ggt gag act gtt cag gaa aga aaa cag aag 853

Ala Phe Gln Lys Tyr Ser Gly Glu Thr Val Gln Glu Arg Lys Gln Lys  
 210 215 220

gat cga aag gca ctc cat gag cta aaa ctg gaa gag tgg aaa ggc aga 901  
 Asp Arg Lys Ala Leu His Glu Leu Lys Leu Glu Glu Trp Lys Gly Arg  
 225 230 235

cta caa gtt act gag cac ctc cct gag aaa att gaa agt agt tta cag 949  
 Leu Gln Val Thr Glu His Leu Pro Glu Lys Ile Glu Ser Ser Leu Gln  
 240 245 250 255

gaa gat gaa cct gag aat gat gct aag aaa att gaa gca ctg cta aac 997  
 Glu Asp Glu Pro Glu Asn Asp Ala Lys Lys Ile Glu Ala Leu Leu Asn  
 260 265 270

ctt cct aga aac cct tca gta ata gat aaa caa gac aag gac tga 1042  
 Leu Pro Arg Asn Pro Ser Val Ile Asp Lys Gln Asp Lys Asp  
 275 280 285

aagtgctctg aacttgaaac tcaactggaga gctgaaggga gctgccatgt ccgatgaatg 1102

ccaacagaca ggccactctt tggtcagcct gctgacaaat ttaagtgctg gtacctgtgg 1162

tggcagtggc ttgctcttgt ctttttcttt tctttttaac taagaatggg gctgttgtac 1222

tctcaacttta cttatccttc aatttaaata catacttatg tttgtattaa tctatcaata 1282

tatgcataca tgaatatatc caccaccta gattttaagc agtaaataaa acatttcgca 1342

aaagatt 1349

<210> 78  
 <211> 285  
 <212> PRT  
 <213> Homo sapiens

<400> 78

Met Glu Val Pro Pro Pro Ala Pro Arg Ser Phe Leu Cys Arg Ala Leu  
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Cys Leu Phe Pro Arg Val Phe Ala Ala Glu Ala Val Thr Ala Asp Ser  
 20 25 30

Glu Val Leu Glu Glu Arg Gln Lys Arg Leu Pro Tyr Val Pro Glu Pro  
 35 40 45

Tyr Tyr Pro Glu Ser Gly Trp Asp Arg Leu Arg Glu Leu Phe Gly Lys  
 50 55 60

Asp Glu Gln Gln Arg Ile Ser Lys Asp Leu Ala Asn Ile Cys Lys Thr  
 65 70 75 80

Ala Ala Thr Ala Gly Ile Ile Gly Trp Val Tyr Gly Gly Ile Pro Ala  
 85 90 95

Phe Ile His Ala Lys Gln Gln Tyr Ile Glu Gln Ser Gln Ala Glu Ile  
 100 105 110

Tyr His Asn Arg Phe Asp Ala Val Gln Ser Ala His Arg Ala Ala Thr  
 115 120 125

Arg Gly Phe Ile Arg Tyr Gly Trp Arg Trp Gly Trp Arg Thr Ala Val  
 130 135 140

Phe Val Thr Ile Phe Asn Thr Val Asn Thr Ser Leu Asn Val Tyr Arg

145		150		155		160
Asn Lys Asp Ala Leu Ser His Phe Val Ile Ala Gly Ala Val Thr Gly						
	165		170			175
Ser Leu Phe Arg Ile Asn Val Gly Leu Arg Gly Leu Val Ala Gly Gly						
	180		185			190
Ile Ile Gly Ala Leu Leu Gly Thr Pro Val Gly Gly Leu Leu Met Ala						
	195		200			205
Phe Gln Lys Tyr Ser Gly Glu Thr Val Gln Glu Arg Lys Gln Lys Asp						
	210		215			220
Arg Lys Ala Leu His Glu Leu Lys Leu Glu Glu Trp Lys Gly Arg Leu						
	225		230			235
Gln Val Thr Glu His Leu Pro Glu Lys Ile Glu Ser Ser Leu Gln Glu						
	245		250			255
Asp Glu Pro Glu Asn Asp Ala Lys Lys Ile Glu Ala Leu Leu Asn Leu						
	260		265			270
Pro Arg Asn Pro Ser Val Ile Asp Lys Gln Asp Lys Asp						
	275		280			285

<210> 79  
 <211> 1355  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (79)..(1068)

<400> 79  
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cgaagccaca caggagcc atg gaa gtg gca gag ccc agc agc ccc act gaa	111
Met Glu Val Ala Glu Pro Ser Ser Pro Thr Glu	
1 5 10	

gag gag gag gag gaa gag gag cac tcg gca gag cct cgg ccc cgc act	159
Glu Glu Glu Glu Glu Glu Glu His Ser Ala Glu Pro Arg Pro Arg Thr	
15 20 25	

cgc tcc aat cct gaa ggg gct gag gac cgg gca gta ggg gca cag gcc	207
Arg Ser Asn Pro Glu Gly Ala Glu Asp Arg Ala Val Gly Ala Gln Ala	
30 35 40	

agc gtg ggc agc cgc agc gag ggt gag ggt gag gcc gcc agt gct gat	255
Ser Val Gly Ser Arg Ser Glu Gly Glu Gly Glu Ala Ala Ser Ala Asp	
45 50 55	

gat ggg agc ctc aac act tca gga gcc gcc cct aag tcc tgg cag gtg	303
Asp Gly Ser Leu Asn Thr Ser Gly Ala Gly Pro Lys Ser Trp Gln Val	
60 65 70 75	

ccc ccg cca gcc cct gag gtc caa att cgg aca cca agg gtc aac tgt	351
Pro Pro Pro Ala Pro Glu Val Gln Ile Arg Thr Pro Arg Val Asn Cys	
80 85 90	

cca gag aaa gtg att atc tgc ctg gac ctg tca gag gaa atg tca ctg	399
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Pro	Glu	Lys	Val	Ile	Ile	Cys	Leu	Asp	Leu	Ser	Glu	Glu	Met	Ser	Leu	
			95					100					105			
cca	aag	ctg	gag	tcg	ttc	aac	ggc	tcc	aaa	acc	aac	gcc	ctc	aat	gtc	447
Pro	Lys	Leu	Glu	Ser	Phe	Asn	Gly	Ser	Lys	Thr	Asn	Ala	Leu	Asn	Val	
		110					115					120				
tcc	cag	aag	atg	att	gag	atg	ttc	gtg	cgg	aca	aaa	cac	aag	atc	gac	495
Ser	Gln	Lys	Met	Ile	Glu	Met	Phe	Val	Arg	Thr	Lys	His	Lys	Ile	Asp	
		125				130					135					
aaa	agc	cac	gag	ttt	gca	ctg	gtg	gtg	gtg	aac	gat	gac	acg	gcc	tgg	543
Lys	Ser	His	Glu	Phe	Ala	Leu	Val	Val	Val	Asn	Asp	Asp	Thr	Ala	Trp	
		140			145					150					155	
ctg	tct	ggc	ctg	acc	tcc	gac	ccc	cgc	gag	ctc	tgt	agc	tgc	ctc	tat	591
Leu	Ser	Gly	Leu	Thr	Ser	Asp	Pro	Arg	Glu	Leu	Cys	Ser	Cys	Leu	Tyr	
				160					165					170		
gat	ctg	gag	acg	gcc	tcc	tgt	tcc	acc	ttc	aat	ctg	gaa	gga	ctt	ttc	639
Asp	Leu	Glu	Thr	Ala	Ser	Cys	Ser	Thr	Phe	Asn	Leu	Glu	Gly	Leu	Phe	
			175					180					185			
agc	ctc	atc	cag	cag	aaa	act	gag	ctt	ccg	gtc	aca	gag	aac	gtg	cag	687
Ser	Leu	Ile	Gln	Gln	Lys	Thr	Glu	Leu	Pro	Val	Thr	Glu	Asn	Val	Gln	
		190					195					200				
acg	att	ccc	ccg	cca	tat	gtg	gtc	cgc	acc	atc	ctt	gtc	tac	agc	cgt	735
Thr	Ile	Pro	Pro	Pro	Tyr	Val	Val	Arg	Thr	Ile	Leu	Val	Tyr	Ser	Arg	
		205				210					215					
cca	cct	tgc	cag	ccc	cag	ttc	tcc	ttg	acg	gag	ccc	atg	aag	aaa	atg	783
Pro	Pro	Cys	Gln	Pro	Gln	Phe	Ser	Leu	Thr	Glu	Pro	Met	Lys	Lys	Met	
		220			225					230					235	
ttc	cag	tgc	cca	tat	ttc	ttc	ttt	gac	gtt	gtt	tac	atc	cac	aat	ggc	831
Phe	Gln	Cys	Pro	Tyr	Phe	Phe	Phe	Asp	Val	Val	Tyr	Ile	His	Asn	Gly	
				240					245					250		
act	gag	gag	aag	gag	gag	gag	atg	agt	tgg	aag	gat	atg	ttt	gcc	ttc	879
Thr	Glu	Glu	Lys	Glu	Glu	Glu	Met	Ser	Trp	Lys	Asp	Met	Phe	Ala	Phe	
			255				260					265				
atg	ggc	agc	ctg	gat	acc	aag	ggt	acc	agc	tac	aaa	tat	gag	gtg	gca	927
Met	Gly	Ser	Leu	Asp	Thr	Lys	Gly	Thr	Ser	Tyr	Lys	Tyr	Glu	Val	Ala	
			270				275					280				
ctg	gct	ggg	cca	gcc	ctg	gag	ttg	cac	aac	tgc	atg	gcg	aaa	ctg	ttg	975
Leu	Ala	Gly	Pro	Ala	Leu	Glu	Leu	His	Asn	Cys	Met	Ala	Lys	Leu	Leu	
		285				290					295					
gcc	cac	ccc	ctg	cag	cgg	cct	tgc	cag	agc	cat	gct	tcc	tac	agc	ctg	1023
Ala	His	Pro	Leu	Gln	Arg	Pro	Cys	Gln	Ser	His	Ala	Ser	Tyr	Ser	Leu	
		300			305					310					315	
ctg	gag	gag	gag	gat	gaa	gcc	att	gag	gtt	gag	gcc	act	gtc	tga		1068
Leu	Glu	Glu	Glu	Asp	Glu	Ala	Ile	Glu	Val	Glu	Ala	Thr	Val			

320

325

accatccctg tacatctgca ccttcttgtg caaggaagtc cttggcctaa agccttggtt 1128  
 ctcaaactgg gttccttggg acctccgggg tggggggggtt ccaggaggca cgtaggggtac 1188  
 cttgcagggt cctaggaggg aaaccaggga ttccaggagg gatcccaggga actgtgggca 1248  
 cccattttct gtgtctccca gccattttcc actcctagtt tgtcatggat aatttttgtt 1308  
 cttccctgtg tgatttttgc catcaaaata aaaatttgag actcgtt 1355

&lt;210&gt; 80

&lt;211&gt; 329

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 80

Met Glu Val Ala Glu Pro Ser Ser Pro Thr Glu Glu Glu Glu Glu Glu  
 1 5 10 15  
 Glu Glu His Ser Ala Glu Pro Arg Pro Arg Thr Arg Ser Asn Pro Glu  
 20 25 30  
 Gly Ala Glu Asp Arg Ala Val Gly Ala Gln Ala Ser Val Gly Ser Arg  
 35 40 45  
 Ser Glu Gly Glu Gly Glu Ala Ala Ser Ala Asp Asp Gly Ser Leu Asn  
 50 55 60  
 Thr Ser Gly Ala Gly Pro Lys Ser Trp Gln Val Pro Pro Pro Ala Pro  
 65 70 75 80  
 Glu Val Gln Ile Arg Thr Pro Arg Val Asn Cys Pro Glu Lys Val Ile  
 85 90 95  
 Ile Cys Leu Asp Leu Ser Glu Glu Met Ser Leu Pro Lys Leu Glu Ser  
 100 105 110  
 Phe Asn Gly Ser Lys Thr Asn Ala Leu Asn Val Ser Gln Lys Met Ile  
 115 120 125  
 Glu Met Phe Val Arg Thr Lys His Lys Ile Asp Lys Ser His Glu Phe  
 130 135 140  
 Ala Leu Val Val Val Asn Asp Asp Thr Ala Trp Leu Ser Gly Leu Thr  
 145 150 155 160  
 Ser Asp Pro Arg Glu Leu Cys Ser Cys Leu Tyr Asp Leu Glu Thr Ala  
 165 170 175  
 Ser Cys Ser Thr Phe Asn Leu Glu Gly Leu Phe Ser Leu Ile Gln Gln  
 180 185 190  
 Lys Thr Glu Leu Pro Val Thr Glu Asn Val Gln Thr Ile Pro Pro Pro  
 195 200 205  
 Tyr Val Val Arg Thr Ile Leu Val Tyr Ser Arg Pro Pro Cys Gln Pro  
 210 215 220  
 Gln Phe Ser Leu Thr Glu Pro Met Lys Lys Met Phe Gln Cys Pro Tyr  
 225 230 235 240  
 Phe Phe Phe Asp Val Val Tyr Ile His Asn Gly Thr Glu Glu Lys Glu  
 245 250 255  
 Glu Glu Met Ser Trp Lys Asp Met Phe Ala Phe Met Gly Ser Leu Asp  
 260 265 270  
 Thr Lys Gly Thr Ser Tyr Lys Tyr Glu Val Ala Leu Ala Gly Pro Ala  
 275 280 285  
 Leu Glu Leu His Asn Cys Met Ala Lys Leu Leu Ala His Pro Leu Gln  
 290 295 300

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 10/25/08 88906880



aga tgc acg ccc aag aat ctt gat tac aag aga gac ttg ttt tgc ctc 532  
Arg Cys Thr Pro Lys Asn Leu Asp Tyr Lys Arg Asp Leu Phe Cys Leu  
155 160 165

agt gtt gaa gcc att gaa agt tat gtt tta ggg tcc tct gaa aag caa 580  
Ser Val Glu Ala Ile Glu Ser Tyr Val Leu Gly Ser Ser Glu Lys Gln  
170 175 180

att gtg tca gaa gat aaa gag ctt ttt aat ctt gaa agc aga gtt gaa 628  
Ile Val Ser Glu Asp Lys Glu Leu Phe Asn Leu Glu Ser Arg Val Glu  
185 190 195 200

ata gaa aag tct cta aca cag atg gaa gat gtc ttg aaa gca tta caa 676  
Ile Glu Lys Ser Leu Thr Gln Met Glu Asp Val Leu Lys Ala Leu Gln  
205 210 215

atg aag ctg tgg gag gcc gaa tcc aaa ttg tcc ttt gcc act tgt aaa 724  
Met Lys Leu Trp Glu Ala Glu Ser Lys Leu Ser Phe Ala Thr Cys Lys  
220 225 230

agc tga actctagtct gtgtcctcca ttctgcccc gcccttctc cccttatttg 780  
Ser

ttaaatgaag caacatagtg agacgtcgtc tctacaaaa aaaaaagaaa aaaaaaatt 840

agccaggcat gcgaaacgct gaggtgggag gatcagatga gcttgggagg ttgaggctgc 900

agtgagcctt ggtcatgcca ctactgcgtt ctagtctggg caacagagtg agaccttctc 960

tcaaaaaaaaa aaccctaaat tgtagaatta cttctatagc tatattttat gataaagaag 1020

tgattgtttc tcaaaatcgc attttaaaga cgttttatgg tacttggttg aattgggact 1080

taggagtttt gattttgata agaaactggg atgattttct gaactttttt tcctctgtat 1140

cacattttatt tactattttt aaaaactttg acatttaaca cttgggacaa cattttattat 1200

aatgataag aaaaatctta gaggtttgtc taccacagc gtcattggaat cttctctgaa 1260

aactaatcca taaagttccc tggagaaatt ggtcagaatg atctgtcaga accatttgaa 1320

aacttgctca agagcagttg cttatatata gtaggatttt actttttcct gcttatgtac 1380

tactatatgc ttaaaaaacc tggaggaata cttaccaaag aggagtaacc atctctgagg 1440

gtgggattct gggggaattt ttgttttttt ctgttttcta taatgtgaaa cttttgtagt 1500

atgtattttt ctaattgaag agaataaaga ttaaaacaaa gtg 1543

<210> 82

<211> 233

<212> PRT

<213> Homo sapiens

<400> 82

Met Ala Gly Val Arg Ser Leu Arg Cys Ser Arg Gly Cys Ala Gly Gly



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Cys Glu Cys Gly Asp Lys Gly Lys Cys Ser Asp Ser Ser Leu Leu Gly			
20	25	30	
Lys Arg Leu Ser Glu Asp Ser Ser Arg His Gln Leu Leu Gln Lys Trp			
35	40	45	
Ala Ser Met Trp Ser Ser Met Ser Glu Asp Ala Ser Val Ala Asp Met			
50	55	60	
Glu Arg Ala Gln Leu Glu Glu Glu Ala Ala Ala Ala Glu Glu Arg Pro			
65	70	75	80
Leu Val Phe Leu Cys Ser Gly Cys Arg Arg Pro Leu Gly Asp Ser Leu			
85	90	95	
Ser Trp Val Ala Ser Gln Glu Asp Thr Asn Cys Ile Leu Leu Arg Cys			
100	105	110	
Val Ser Cys Asn Val Ser Val Asp Lys Glu Gln Lys Leu Ser Lys Arg			
115	120	125	
Glu Lys Glu Asn Gly Cys Val Leu Glu Thr Leu Cys Cys Ala Gly Cys			
130	135	140	
Ser Leu Asn Leu Gly Tyr Val Tyr Arg Cys Thr Pro Lys Asn Leu Asp			
145	150	155	160
Tyr Lys Arg Asp Leu Phe Cys Leu Ser Val Glu Ala Ile Glu Ser Tyr			
165	170	175	
Val Leu Gly Ser Ser Glu Lys Gln Ile Val Ser Glu Asp Lys Glu Leu			
180	185	190	
Phe Asn Leu Glu Ser Arg Val Glu Ile Glu Lys Ser Leu Thr Gln Met			
195	200	205	
Glu Asp Val Leu Lys Ala Leu Gln Met Lys Leu Trp Glu Ala Glu Ser			
210	215	220	
Lys Leu Ser Phe Ala Thr Cys Lys Ser			
225	230		

<210> 83  
 <211> 1436  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (31)..(582)

<400> 83  
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ttg tgg cgg ctg cag aag ctg ccg gcc gag ctg ggc ccg cag ctt ctt 102  
 Leu Trp Arg Leu Gln Lys Leu Pro Ala Glu Leu Gly Pro Gln Leu Leu  
 10 15 20

cac aaa ata att gat ggc att tgt ggt cga gct tat cct gtg tac caa 150  
 His Lys Ile Ile Asp Gly Ile Cys Gly Arg Ala Tyr Pro Val Tyr Gln  
 25 30 35 40

gat tat cac act gtt tgg gaa tca gaa gaa tgg atg cac gtt tta gaa 198  
 Asp Tyr His Thr Val Trp Glu Ser Glu Glu Trp Met His Val Leu Glu  
 45 50 55

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gat att gcc aaa ttt ttc aaa gcc ata gtt ggt aaa aac tta cct gat	246
Asp Ile Ala Lys Phe Phe Lys Ala Ile Val Gly Lys Asn Leu Pro Asp	
60 65 70	
gaa gag ata ttt cag cag ttg aat cag ttg aat tca ctt cat caa gaa	294
Glu Glu Ile Phe Gln Gln Leu Asn Gln Leu Asn Ser Leu His Gln Glu	
75 80 85	
act atc atg aaa tgc gtg aaa agt agg aaa gat gaa atc aaa cag gct	342
Thr Ile Met Lys Cys Val Lys Ser Arg Lys Asp Glu Ile Lys Gln Ala	
90 95 100	
ctg tca aga gaa ata gtt gct att tcc tct gca cag cta cag gat ttt	390
Leu Ser Arg Glu Ile Val Ala Ile Ser Ser Ala Gln Leu Gln Asp Phe	
105 110 115 120	
gat tgg cag gta aag ctt gca ctt tcc agt gac aag att gct gca tta	438
Asp Trp Gln Val Lys Leu Ala Leu Ser Ser Asp Lys Ile Ala Ala Leu	
125 130 135	
cga atg cca ctt tta agc ctg cat cta gat gta aaa gaa aat ggt gaa	486
Arg Met Pro Leu Leu Ser Leu His Leu Asp Val Lys Glu Asn Gly Glu	
140 145 150	
gta aaa cct tat tct att gaa atg agt aga gag gag ctg cag aat cta	534
Val Lys Pro Tyr Ser Ile Glu Met Ser Arg Glu Glu Leu Gln Asn Leu	
155 160 165	
ata cag tcc ttg gaa gca gcg aat aag gtg gtc ctg cag ttg aaa taa	582
Ile Gln Ser Leu Glu Ala Ala Asn Lys Val Val Leu Gln Leu Lys	
170 175 180	
ctggaaatga tgaataccag tcctatcaga ttttattgct ccaacttata tggcagagtg	642
aatactgcgt gttcagaaac cttgtgatgt cttgactgtt gcaccaggct gagaaagcag	702
caatattgat attataaaga taaaaattta tcaacattcc ttaacaggaa attacatggt	762
tgagaggaaa tgcataaaat gaaagatgaa aaatctatag tagcagttta tattttcatg	822
attgttttgc ctcatattt aaatatattga gaaatctttg gagatacata gttttattga	882
aagctaaaaa taggtttctaa agtaatgtaa aaatataaag cacaaatata cttgaatatt	942
gcttaaagaa ttgtgtgaat agcaacatat attatggata tatactttgt gatattttta	1002
aaaaataatt ttttcaaaga atgtataagc tgcatatata actcaggaga ttccatgtct	1062
ttctcatatt tcagaggaaa gattataaaa tataaaattt cttagagaac acctctttgt	1122
cagagataaa caagaacaaa tactctaaac ttatgtgaac agttttgagt ttatgaattc	1182
tagaaactaa aatcaagaat acagaaaaat gaaaataaca ttttacttct gcgcttctat	1242
gtttgggaaa cattgctctg ataaaaaata gctgtcatta tgcagtgtgt atattcaa	1302
atgagataag actatgtaca catccacttt tgttaataaa ctcaatattg aatacttttg	1362

gatgttaaatt tcattggaaa aacaaacccat ttgtaacctc agttaacttt aacaacaagc 1422  
attctgagca aatg 1436

<210> 84  
<211> 183  
<212> PRT  
<213> Homo sapiens

<400> 84  
Met Glu Pro Glu Glu Gly Thr Pro Leu Trp Arg Leu Gln Lys Leu Pro  
1 5 10 15  
Ala Glu Leu Gly Pro Gln Leu Leu His Lys Ile Ile Asp Gly Ile Cys  
20 25 30  
Gly Arg Ala Tyr Pro Val Tyr Gln Asp Tyr His Thr Val Trp Glu Ser  
35 40 45  
Glu Glu Trp Met His Val Leu Glu Asp Ile Ala Lys Phe Phe Lys Ala  
50 55 60  
Ile Val Gly Lys Asn Leu Pro Asp Glu Glu Ile Phe Gln Gln Leu Asn  
65 70 75 80  
Gln Leu Asn Ser Leu His Gln Glu Thr Ile Met Lys Cys Val Lys Ser  
85 90 95  
Arg Lys Asp Glu Ile Lys Gln Ala Leu Ser Arg Glu Ile Val Ala Ile  
100 105 110  
Ser Ser Ala Gln Leu Gln Asp Phe Asp Trp Gln Val Lys Leu Ala Leu  
115 120 125  
Ser Ser Asp Lys Ile Ala Ala Leu Arg Met Pro Leu Leu Ser Leu His  
130 135 140  
Leu Asp Val Lys Glu Asn Gly Glu Val Lys Pro Tyr Ser Ile Glu Met  
145 150 155 160  
Ser Arg Glu Glu Leu Gln Asn Leu Ile Gln Ser Leu Glu Ala Ala Asn  
165 170 175  
Lys Val Val Leu Gln Leu Lys  
180

<210> 85  
<211> 1357  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (102)..(1244)

<400> 85  
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tccgcgggac ggggagaaaag agagagcgcg aaagagagag g atg tct ctc tca gac 116  
Met Ser Leu Ser Asp  
1 5  
tgg cac ctg gcg gtg aag ctg gct gac cag cca ctt act cca aag tct 164  
Trp His Leu Ala Val Lys Leu Ala Asp Gln Pro Leu Thr Pro Lys Ser  
10 15 20

att ctt cgg ttg cca gag aca gaa ctg gga gaa tac tcg cta ggg ggc	212
Ile Leu Arg Leu Pro Glu Thr Glu Leu Gly Glu Tyr Ser Leu Gly Gly	
25 30 35	
tat agt att tca ttt ctg aag cag ctt att gct ggc aaa ctc cag gag	260
Tyr Ser Ile Ser Phe Leu Lys Gln Leu Ile Ala Gly Lys Leu Gln Glu	
40 45 50	
tct gtt cca gac cct gag ctg att gat ctg atc tac tgt ggt cgg aag	308
Ser Val Pro Asp Pro Glu Leu Ile Asp Leu Ile Tyr Cys Gly Arg Lys	
55 60 65	
cta aaa gat gac cag aca ctt gac ttc tat ggc att caa cct ggg tcc	356
Leu Lys Asp Asp Gln Thr Leu Asp Phe Tyr Gly Ile Gln Pro Gly Ser	
70 75 80 85	
act gtc cat gtt ctg cga aag tcc tgg cct gaa cct gat cag aaa ccg	404
Thr Val His Val Leu Arg Lys Ser Trp Pro Glu Pro Asp Gln Lys Pro	
90 95 100	
gaa cct gtg gac aaa gtg gct gcc atg aga gag ttc cgg gtg ttg cac	452
Glu Pro Val Asp Lys Val Ala Ala Met Arg Glu Phe Arg Val Leu His	
105 110 115	
act gcc ctg cac agc agc tcc tct tac agg gag gcg gtc ttt aag atg	500
Thr Ala Leu His Ser Ser Ser Ser Tyr Arg Glu Ala Val Phe Lys Met	
120 125 130	
ctc agc aat aag gag tct ctg gat cag atc att gtg gcc acc cca ggc	548
Leu Ser Asn Lys Glu Ser Leu Asp Gln Ile Ile Val Ala Thr Pro Gly	
135 140 145	
ctc agc agt gac cct att gct ctt ggg gtt ctc cag gac aag gac ctc	596
Leu Ser Ser Asp Pro Ile Ala Leu Gly Val Leu Gln Asp Lys Asp Leu	
150 155 160 165	
ttc tct gtc ttc gct gat ccc aat atg ctt gat acg ttg gtg cct gct	644
Phe Ser Val Phe Ala Asp Pro Asn Met Leu Asp Thr Leu Val Pro Ala	
170 175 180	
cac cca gcc ctc gtc aat gcc att gtc ctg gtt ctg cac tcc gta gca	692
His Pro Ala Leu Val Asn Ala Ile Val Leu Val Leu His Ser Val Ala	
185 190 195	
ggc agt gcc cca atg cct ggg act gac tcc tct tcc cgg agc atg ccc	740
Gly Ser Ala Pro Met Pro Gly Thr Asp Ser Ser Ser Arg Ser Met Pro	
200 205 210	
tcc agc tca tac cgg gat atg cca ggt ggc ttc ctg ttt gaa ggg ctc	788
Ser Ser Ser Tyr Arg Asp Met Pro Gly Gly Phe Leu Phe Glu Gly Leu	
215 220 225	
tca gat gat gag gat gac ttt cac cca aac acc agg tcc aca ccc tct	836
Ser Asp Asp Glu Asp Asp Phe His Pro Asn Thr Arg Ser Thr Pro Ser	
230 235 240 245	

agc agt act ccc agc tcc cgc cca gcc tcc ctg ggg tac agt gga gct 884  
 Ser Ser Thr Pro Ser Ser Arg Pro Ala Ser Leu Gly Tyr Ser Gly Ala  
 250 255 260

gct ggg ccc cgg ccc atc acc cag agt gag ctg gcc acc gcc ttg gcc 932  
 Ala Gly Pro Arg Pro Ile Thr Gln Ser Glu Leu Ala Thr Ala Leu Ala  
 265 270 275

ctg gcc agc act ccg gag agc agc tct cac aca ccg act cct ggc acc 980  
 Leu Ala Ser Thr Pro Glu Ser Ser Ser His Thr Pro Thr Pro Gly Thr  
 280 285 290

cag ggt cat tcc tca ggg acc tca cca atg tcc tct ggt gtc cag tca 1028  
 Gln Gly His Ser Ser Gly Thr Ser Pro Met Ser Ser Gly Val Gln Ser  
 295 300 305

ggg acg ccc atc acc aat gat ctc ttc agc caa gcc cta cag cat gcc 1076  
 Gly Thr Pro Ile Thr Asn Asp Leu Phe Ser Gln Ala Leu Gln His Ala  
 310 315 320 325

ctt cag gcc tct ggg cag ccc agc ctt cag agc cag tgg cag ccc cag 1124  
 Leu Gln Ala Ser Gly Gln Pro Ser Leu Gln Ser Gln Trp Gln Pro Gln  
 330 335 340

ctg cag cag cta cgt gac atg ggc atc cag gac gat gag ctg agc ctg 1172  
 Leu Gln Gln Leu Arg Asp Met Gly Ile Gln Asp Asp Glu Leu Ser Leu  
 345 350 355

cgg gcc ctg cag gcc acc ggt ggg gac atc caa gca gcc ctg gag ctc 1220  
 Arg Ala Leu Gln Ala Thr Gly Gly Asp Ile Gln Ala Ala Leu Glu Leu  
 360 365 370

atc ttt gct gga gga gcc cca tga actccctgct tcccctgaac ccccagcaag 1274  
 Ile Phe Ala Gly Gly Ala Pro  
 375 380

ttgcagaggc tactgccctt gggaggcact catgaagggtg cctccatctc tcccttcccc 1334

aatatacctg atggtcaact ctc 1357

<210> 86  
 <211> 380  
 <212> PRT  
 <213> Homo sapiens

<400> 86  
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 20 25 30  
 Tyr Ser Leu Gly Gly Tyr Ser Ile Ser Phe Leu Lys Gln Leu Ile Ala  
 35 40 45  
 Gly Lys Leu Gln Glu Ser Val Pro Asp Pro Glu Leu Ile Asp Leu Ile  
 50 55 60  
 Tyr Cys Gly Arg Lys Leu Lys Asp Asp Gln Thr Leu Asp Phe Tyr Gly  
 65 70 75 80

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Ile Gln Pro Gly Ser Thr Val His Val Leu Arg Lys Ser Trp Pro Glu
      85                      90                      95
Pro Asp Gln Lys Pro Glu Pro Val Asp Lys Val Ala Ala Met Arg Glu
      100                    105                    110
Phe Arg Val Leu His Thr Ala Leu His Ser Ser Ser Tyr Arg Glu
      115                    120                    125
Ala Val Phe Lys Met Leu Ser Asn Lys Glu Ser Leu Asp Gln Ile Ile
      130                    135                    140
Val Ala Thr Pro Gly Leu Ser Ser Asp Pro Ile Ala Leu Gly Val Leu
      145                    150                    155                    160
Gln Asp Lys Asp Leu Phe Ser Val Phe Ala Asp Pro Asn Met Leu Asp
      165                    170                    175
Thr Leu Val Pro Ala His Pro Ala Leu Val Asn Ala Ile Val Leu Val
      180                    185                    190
Leu His Ser Val Ala Gly Ser Ala Pro Met Pro Gly Thr Asp Ser Ser
      195                    200                    205
Ser Arg Ser Met Pro Ser Ser Ser Tyr Arg Asp Met Pro Gly Gly Phe
      210                    215                    220
Leu Phe Glu Gly Leu Ser Asp Asp Glu Asp Asp Phe His Pro Asn Thr
      225                    230                    235                    240
Arg Ser Thr Pro Ser Ser Ser Thr Pro Ser Ser Arg Pro Ala Ser Leu
      245                    250                    255
Gly Tyr Ser Gly Ala Ala Gly Pro Arg Pro Ile Thr Gln Ser Glu Leu
      260                    265                    270
Ala Thr Ala Leu Ala Leu Ala Ser Thr Pro Glu Ser Ser Ser His Thr
      275                    280                    285
Pro Thr Pro Gly Thr Gln Gly His Ser Ser Gly Thr Ser Pro Met Ser
      290                    295                    300
Ser Gly Val Gln Ser Gly Thr Pro Ile Thr Asn Asp Leu Phe Ser Gln
      305                    310                    315                    320
Ala Leu Gln His Ala Leu Gln Ala Ser Gly Gln Pro Ser Leu Gln Ser
      325                    330                    335
Gln Trp Gln Pro Gln Leu Gln Gln Leu Arg Asp Met Gly Ile Gln Asp
      340                    345                    350
Asp Glu Leu Ser Leu Arg Ala Leu Gln Ala Thr Gly Gly Asp Ile Gln
      355                    360                    365
Ala Ala Leu Glu Leu Ile Phe Ala Gly Gly Ala Pro
      370                    375                    380

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<210> 87  
 <211> 1399  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (74)..(856)

<400> 87  
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gaggtatatc tcc atg aat aac cta aat gat ccc cca aat tgg aat atc 109  
 Met Asn Asn Leu Asn Asp Pro Pro Asn Trp Asn Ile  
 1 5 10

cgg cct aat tcc agg gcg gat ggt ggt gat gga agc agg tgg aat tat	157
Arg Pro Asn Ser Arg Ala Asp Gly Gly Asp Gly Ser Arg Trp Asn Tyr	
15 20 25	
gcc ctg ttg gtt cca atg ctg gga ttg gct gct ttt cgt tgg att tgg	205
Ala Leu Leu Val Pro Met Leu Gly Leu Ala Ala Phe Arg Trp Ile Trp	
30 35 40	
tct agg gag tcc cag aaa gaa gta gaa aaa gag aga gaa gcc tac cgt	253
Ser Arg Glu Ser Gln Lys Glu Val Glu Lys Glu Arg Glu Ala Tyr Arg	
45 50 55 60	
cgg aga act gct gct ttt caa cag gat ctg gaa gcc aag tac cac gcc	301
Arg Arg Thr Ala Ala Phe Gln Gln Asp Leu Glu Ala Lys Tyr His Ala	
65 70 75	
atg atc tca gaa aat cgg cgt gct gtc gct cag ttg tcc ttg gaa ctc	349
Met Ile Ser Glu Asn Arg Arg Ala Val Ala Gln Leu Ser Leu Glu Leu	
80 85 90	
gaa aag gaa caa aac aga act gct agt tac cga gaa gcc ctt atc tct	397
Glu Lys Glu Gln Asn Arg Thr Ala Ser Tyr Arg Glu Ala Leu Ile Ser	
95 100 105	
cag gga cgc aag ttg gta gaa gaa aag aag ctt ctg gaa cag gaa cgg	445
Gln Gly Arg Lys Leu Val Glu Glu Lys Lys Leu Glu Glu Gln Glu Arg	
110 115 120	
gcc cag gtg atg caa gaa aaa aga cag gtg cag cct ttg aga agt gcg	493
Ala Gln Val Met Gln Glu Lys Arg Gln Val Gln Pro Leu Arg Ser Ala	
125 130 135 140	
tat ttg agc tgc ctg caa agg gaa gaa aac tgg caa agg aga gcc agg	541
Tyr Leu Ser Cys Leu Gln Arg Glu Glu Asn Trp Gln Arg Arg Ala Arg	
145 150 155	
ctt ttg ctg aaa gaa ttt gaa gct gtt ctc aca gaa aga cag aat atc	589
Leu Leu Leu Lys Glu Phe Glu Ala Val Leu Thr Glu Arg Gln Asn Ile	
160 165 170	
tac tgc agt ctg ttt ctt cct cgc agc aag cgg ctg gag ata gag aag	637
Tyr Cys Ser Leu Phe Leu Pro Arg Ser Lys Arg Leu Glu Ile Glu Lys	
175 180 185	
agc tta ctg gtg cga gcg tcc gtc gac ccc gtc gcc gct gac cta gag	685
Ser Leu Leu Val Arg Ala Ser Val Asp Pro Val Ala Ala Asp Leu Glu	
190 195 200	
atg gca gcc ggt ctc acc gac ata ttt cag cat gat aca tac tgt ggt	733
Met Ala Ala Gly Leu Thr Asp Ile Phe Gln His Asp Thr Tyr Cys Gly	
205 210 215 220	
gat gtc tgg aac acc aac aaa cgc cag aat ggc aga ctc atg tgg ctc	781
Asp Val Trp Asn Thr Asn Lys Arg Gln Asn Gly Arg Leu Met Trp Leu	
225 230 235	
tat ctc aaa tac tgg gaa ctc gtt gtc gaa ctg aag aag ttt aag aga	829

09890688-092701

Tyr Leu Lys Tyr Trp Glu Leu Val Val Glu Leu Lys Lys Phe Lys Arg  
240 245 250

gta gag gaa gcc ata cta gaa aag taa gacaagagtg aaatcaaact 876  
Val Glu Glu Ala Ile Leu Glu Lys  
255 260

gcttttagtg actcgaggcc aggcagtcac gcgccttctg ggtctccggc gtcttccggt 936  
cccgtgctgc ccgtgtcatg gccacaccgt cacccttcag cagcgacctc cactcccggc 996  
accgtctgag cagaagtgc ccgaagcctc agagacagag ggtctcctcc cgatgctctg 1056  
ccgctgttgg ggatatgggt tcttgaagca ttttaggct gccagtattg tattaagcag 1116  
aacagtataa cctcgtatct tagctccagg gtaaaaatgg ttttttaaaa agtcaaatac 1176  
aatactggtc cttagcacia gtaattttct gtctgtttca tcaactcccta aatactttct 1236  
cctcaaatta tttttctctg tcaccagatt acattaagaa tttgtcagat aatgtgtaga 1296  
actgcataac aggtaataga aagtagtaat attatattat caagggttta tatttttaaag 1356  
atctctctca ctccataaag gggaaatacc aagtgtttct tgt 1399

<210> 88  
<211> 260  
<212> PRT  
<213> Homo sapiens

<400> 88  
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1 5 10 15  
Arg Ala Asp Gly Gly Asp Gly Ser Arg Trp Asn Tyr Ala Leu Leu Val  
20 25 30  
Pro Met Leu Gly Leu Ala Ala Phe Arg Trp Ile Trp Ser Arg Glu Ser  
35 40 45  
Gln Lys Glu Val Glu Lys Glu Arg Glu Ala Tyr Arg Arg Arg Thr Ala  
50 55 60  
Ala Phe Gln Gln Asp Leu Glu Ala Lys Tyr His Ala Met Ile Ser Glu  
65 70 75 80  
Asn Arg Arg Ala Val Ala Gln Leu Ser Leu Glu Leu Glu Lys Glu Gln  
85 90 95  
Asn Arg Thr Ala Ser Tyr Arg Glu Ala Leu Ile Ser Gln Gly Arg Lys  
100 105 110  
Leu Val Glu Glu Lys Lys Leu Leu Glu Gln Glu Arg Ala Gln Val Met  
115 120 125  
Gln Glu Lys Arg Gln Val Gln Pro Leu Arg Ser Ala Tyr Leu Ser Cys  
130 135 140  
Leu Gln Arg Glu Glu Asn Trp Gln Arg Arg Ala Arg Leu Leu Leu Lys  
145 150 155 160  
Glu Phe Glu Ala Val Leu Thr Glu Arg Gln Asn Ile Tyr Cys Ser Leu  
165 170 175  
Phe Leu Pro Arg Ser Lys Arg Leu Glu Ile Glu Lys Ser Leu Leu Val  
180 185 190  
Arg Ala Ser Val Asp Pro Val Ala Ala Asp Leu Glu Met Ala Ala Gly



		195						200						205								
Leu	Thr	Asp	Ile	Phe	Gln	His	Asp	Thr	Tyr	Cys	Gly	Asp	Val	Trp	Asn							
		210						215						220								
Thr	Asn	Lys	Arg	Gln	Asn	Gly	Arg	Leu	Met	Trp	Leu	Tyr	Leu	Lys	Tyr							
225					230						235						240					
Trp	Glu	Leu	Val	Val	Glu	Leu	Lys	Lys	Phe	Lys	Arg	Val	Glu	Glu	Ala							
				245						250						255						
Ile	Leu	Glu	Lys																			
			260																			

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<210> 89
<211> 1119
<212> DNA
<213> Homo sapiens
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09890688-092701

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ctc gca tcc tgc cag tac tac ttt gag aag atc cac cca ccg ggg gaa 556
Leu Ala Ser Cys Gln Tyr Tyr Phe Glu Lys Ile His Pro Pro Gly Glu
120 125 130 135

cgc agg gct ccc cag tac acg ttt ggc tac cgg cgc cca tac aga gtg 604
Arg Arg Ala Pro Gln Tyr Thr Phe Gly Tyr Arg Arg Pro Tyr Arg Val
140 145 150

atg gac ctc aac ccg gct ccc aac cag tac cag atg cca ctc ttg ctg 652
Met Asp Leu Asn Pro Ala Pro Asn Gln Tyr Gln Met Pro Leu Leu Leu
155 160 165

ggg ccc aac acc cct gtc agc cga gct gct ccc tgc tac agt ctg gcc 700
Gly Pro Asn Thr Pro Val Ser Arg Ala Ala Pro Cys Tyr Ser Leu Ala
170 175 180

tcc agg gac aag aac tgg ttc tac aag gag gat gtg gca gga ggc cct 748
Ser Arg Asp Lys Asn Trp Phe Tyr Lys Glu Asp Val Ala Gly Gly Pro
185 190 195

gga cct acc acg tac gcc cga cct gag cca tcc atc tat cag aac cgc 796
Gly Pro Thr Thr Tyr Ala Arg Pro Glu Pro Ser Ile Tyr Gln Asn Arg
200 205 210 215

agc cct act tac agc atg gcc aag cgc ttc gcc tac cct ctg gac ctc 844
Ser Pro Thr Tyr Ser Met Ala Lys Arg Phe Ala Tyr Pro Leu Asp Leu
220 225 230

acg cca cgg cct ggc ccc ggc tcc cac gag gtc cag cag gtc act gtg 892
Thr Pro Arg Pro Gly Pro Gly Ser His Glu Val Gln Gln Val Thr Val
235 240 245

cac aag ccc cac atc cct gct ttc acc atg ggc atc aag cac tca ctc 940
His Lys Pro His Ile Pro Ala Phe Thr Met Gly Ile Lys His Ser Leu
250 255 260

cac ctg tgc cca ctg gtc atc gac att cgt gac tga ggccctctt 986
His Leu Cys Pro Leu Val Ile Asp Ile Arg Asp
265 270

ggggcactca ctgccctca tccccagaaa ttatttttct acaccaaatt gagcaatttg 1046

accaagattt ctagtagcag agccggtacc tgctgagtgt ccggcacaca gaagacatta 1106

gagatacatt ttc 1119

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<210> 90  
 <211> 274  
 <212> PRT  
 <213> Homo sapiens

<400> 90  
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 1 5 10 15  
 Pro Glu Lys Glu Pro Leu Pro Ser Arg Gln Glu Val Lys Gln Thr Pro

[illegible]

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<210> 91
<211> 540
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> (133) .. (438)
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agtgtggttag gtaacgggtcc tcagcgcaag ggtcatttcg tcgctgggaa gggacgcccc 120
tcgcccgcgg tg atg gtg gtt agc aag atg aac aaa gat gcg cag atg aga 171
      Met Val Val Ser Lys Met Asn Lys Asp Ala Gln Met Arg
            1             5             10

gca gcg att aac caa aag ttg ata gaa act gga gaa aga gaa cgc ctc 219
Ala Ala Ile Asn Gln Lys Leu Ile Glu Thr Gly Glu Arg Glu Arg Leu
      15             20             25

aaa gag ttg ctg aga gct aaa tta att gaa tgt ggc tgg aag gat cag 267

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Lys Glu Leu Leu Arg Ala Lys Leu Ile Glu Cys Gly Trp Lys Asp Gln  
 30 35 40 45

ttg aag gca cac tgt aaa gag gta att aaa gaa aaa gga cta gaa cac 315  
 Leu Lys Ala His Cys Lys Glu Val Ile Lys Glu Lys Gly Leu Glu His  
 50 55 60

gtt act gtt gat gac ttg gtg gct gaa atc act cca aaa ggc aga gcc 363  
 Val Thr Val Asp Asp Leu Val Ala Glu Ile Thr Pro Lys Gly Arg Ala  
 65 70 75

ctg gta cct gac agt gta aag aag gag ctc cta caa aga ata aga aca 411  
 Leu Val Pro Asp Ser Val Lys Lys Glu Leu Leu Gln Arg Ile Arg Thr  
 80 85 90

ttc ctt gct cag cat gcc agc ctt taa gattgaatta gattgtgttg 458  
 Phe Leu Ala Gln His Ala Ser Leu  
 95 100

ttgtggtttt atttctgaaa gtaaaacttg ccataaatta gaaaacaatt tcccaaaata 518

aaatcctttt ttgtatgatg gt 540

<210> 92  
 <211> 101  
 <212> PRT  
 <213> Homo sapiens

<400> 92  
 Met Val Val Ser Lys Met Asn Lys Asp Ala Gln Met Arg Ala Ala Ile  
 1 5 10 15  
 Asn Gln Lys Leu Ile Glu Thr Gly Glu Arg Glu Arg Leu Lys Glu Leu  
 20 25 30  
 Leu Arg Ala Lys Leu Ile Glu Cys Gly Trp Lys Asp Gln Leu Lys Ala  
 35 40 45  
 His Cys Lys Glu Val Ile Lys Glu Lys Gly Leu Glu His Val Thr Val  
 50 55 60  
 Asp Asp Leu Val Ala Glu Ile Thr Pro Lys Gly Arg Ala Leu Val Pro  
 65 70 75 80  
 Asp Ser Val Lys Lys Glu Leu Leu Gln Arg Ile Arg Thr Phe Leu Ala  
 85 90 95  
 Gln His Ala Ser Leu  
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<210> 93  
 <211> 1059  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (33)..(869)

<400> 93  
 gagttcctag taaagtggcg ggagccgcag ct atg gag ccg cag gag gag aga 53

09890688-092701

	Met	Glu	Pro	Gln	Glu	Glu	Arg	
	1				5			
gaa acg cag gtt gct gcg tgg tta aaa aaa ata ttt gga gat cat cct 101								
Glu Thr Gln Val Ala Ala Trp Leu Lys Lys Ile Phe Gly Asp His Pro								
10 15 20								
att cca cag tat gag gtg aac cca cgg acc aca gag att tta cat cac 149								
Ile Pro Gln Tyr Glu Val Asn Pro Arg Thr Thr Glu Ile Leu His His								
25 30 35								
ctt tca gaa cgc aac agg gtc cgg gac agg gat gtc tac ctg gta ata 197								
Leu Ser Glu Arg Asn Arg Val Arg Asp Arg Asp Val Tyr Leu Val Ile								
40 45 50 55								
gag gac ttg aag cag aaa gca agt gaa tac gag tca gaa gcc aag tat 245								
Glu Asp Leu Lys Gln Lys Ala Ser Glu Tyr Glu Ser Glu Ala Lys Tyr								
60 65 70								
ctt caa gac ctt ctc atg gag agt gtg aat ttt tcc ccc gcc aat ctc 293								
Leu Gln Asp Leu Leu Met Glu Ser Val Asn Phe Ser Pro Ala Asn Leu								
75 80 85								
tct agc act ggt tcc agg tat ctg aat gct ttg gtt gac agt gcg gtg 341								
Ser Ser Thr Gly Ser Arg Tyr Leu Asn Ala Leu Val Asp Ser Ala Val								
90 95 100								
gcc ctt gaa aca aag gat acc tcg cta gct agt ttt atc cct gca gtg 389								
Ala Leu Glu Thr Lys Asp Thr Ser Leu Ala Ser Phe Ile Pro Ala Val								
105 110 115								
aat gat ttg acc tct gat ctc ttt cgt acc aaa tcc aaa agt gaa gaa 437								
Asn Asp Leu Thr Ser Asp Leu Phe Arg Thr Lys Ser Lys Ser Glu Glu								
120 125 130 135								
atc aag att gaa ctg gaa aaa ctt gaa aaa aat tta act gca act tta 485								
Ile Lys Ile Glu Leu Glu Lys Leu Glu Lys Asn Leu Thr Ala Thr Leu								
140 145 150								
gta tta gaa aaa tgt cta caa gag gat gtc aag aaa gca gag ttg cat 533								
Val Leu Glu Lys Cys Leu Gln Glu Asp Val Lys Lys Ala Glu Leu His								
155 160 165								
ctg tct aca gaa agg gcc aaa gtt gat aat cgt cgt cag aac atg gac 581								
Leu Ser Thr Glu Arg Ala Lys Val Asp Asn Arg Arg Gln Asn Met Asp								
170 175 180								
ttt cta aaa gca aag tca gag gaa ttc aga ttt gga atc aag gct gca 629								
Phe Leu Lys Ala Lys Ser Glu Glu Phe Arg Phe Gly Ile Lys Ala Ala								
185 190 195								
gag gag caa ctt tca gcc aga ggc atg gat gct tct ctg tct cat cag 677								
Glu Glu Gln Leu Ser Ala Arg Gly Met Asp Ala Ser Leu Ser His Gln								
200 205 210 215								
tcc tta gta gca cta tca gag aaa ctg gca aga tta aag caa cag act 725								
Ser Leu Val Ala Leu Ser Glu Lys Leu Ala Arg Leu Lys Gln Gln Thr								

220	225	230	
ata cct ttg aag aaa aaa ttg gag tcc tat tta gac tta atg ccg aat	773		
Ile Pro Leu Lys Lys Lys Leu Glu Ser Tyr Leu Asp Leu Met Pro Asn			
235 240 245			
ccg tct ctt gct caa gtg aaa att gaa gaa gca aag cga gaa cta gat	821		
Pro Ser Leu Ala Gln Val Lys Ile Glu Glu Ala Lys Arg Glu Leu Asp			
250 255 260			
agc att gaa gct gaa ctt aca aga aga gta gac atg atg gaa ctg tga	869		
Ser Ile Glu Ala Glu Leu Thr Arg Arg Val Asp Met Met Glu Leu			
265 270 275			
caaaagccaa ataaacatcc ttttccctaa caaagtaaat tgaataggac tttacagagt 929			
tctttttcct ctgggcattt cctaataaca aaactttctg tgttcttaga ttacagaata 989			
tcataattga tagaatatgg tttcttactg tgtgttgcat ttttgtgcc aaatacatag 1049			
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<210> 94			
<211> 278			
<212> PRT			
<213> Homo sapiens			
<400> 94			
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1 5 10 15			
Lys Ile Phe Gly Asp His Pro Ile Pro Gln Tyr Glu Val Asn Pro Arg			
20 25 30			
Thr Thr Glu Ile Leu His His Leu Ser Glu Arg Asn Arg Val Arg Asp			
35 40 45			
Arg Asp Val Tyr Leu Val Ile Glu Asp Leu Lys Gln Lys Ala Ser Glu			
50 55 60			
Tyr Glu Ser Glu Ala Lys Tyr Leu Gln Asp Leu Leu Met Glu Ser Val			
65 70 75 80			
Asn Phe Ser Pro Ala Asn Leu Ser Ser Thr Gly Ser Arg Tyr Leu Asn			
85 90 95			
Ala Leu Val Asp Ser Ala Val Ala Leu Glu Thr Lys Asp Thr Ser Leu			
100 105 110			
Ala Ser Phe Ile Pro Ala Val Asn Asp Leu Thr Ser Asp Leu Phe Arg			
115 120 125			
Thr Lys Ser Lys Ser Glu Glu Ile Lys Ile Glu Leu Glu Lys Leu Glu			
130 135 140			
Lys Asn Leu Thr Ala Thr Leu Val Leu Glu Lys Cys Leu Gln Glu Asp			
145 150 155 160			
Val Lys Lys Ala Glu Leu His Leu Ser Thr Glu Arg Ala Lys Val Asp			
165 170 175			
Asn Arg Arg Gln Asn Met Asp Phe Leu Lys Ala Lys Ser Glu Glu Phe			
180 185 190			
Arg Phe Gly Ile Lys Ala Ala Glu Glu Gln Leu Ser Ala Arg Gly Met			
195 200 205			
Asp Ala Ser Leu Ser His Gln Ser Leu Val Ala Leu Ser Glu Lys Leu			
210 215 220			

Ala Arg Leu Lys Gln Gln Thr Ile Pro Leu Lys Lys Lys Leu Glu Ser  
 225 230 235 240  
 Tyr Leu Asp Leu Met Pro Asn Pro Ser Leu Ala Gln Val Lys Ile Glu  
 245 250 255  
 Glu Ala Lys Arg Glu Leu Asp Ser Ile Glu Ala Glu Leu Thr Arg Arg  
 260 265 270  
 Val Asp Met Met Glu Leu  
 275

<210> 95  
 <211> 782  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (103)..(384)

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 Met Ser Gly Leu  
 1  
 cgc gtc tac agc acg tcg gtc acc ggc tcc cgc gaa atc aag tcc cag 162  
 Arg Val Tyr Ser Thr Ser Val Thr Gly Ser Arg Glu Ile Lys Ser Gln  
 5 10 15 20  
 cag agc gag gtg acc cga atc ctg gat ggg aag cgc atc caa tac cag 210  
 Gln Ser Glu Val Thr Arg Ile Leu Asp Gly Lys Arg Ile Gln Tyr Gln  
 25 30 35  
 cta gtg gac atc tcc cag gac aac gcc ctg agg gat gag atg cga gcc 258  
 Leu Val Asp Ile Ser Gln Asp Asn Ala Leu Arg Asp Glu Met Arg Ala  
 40 45 50  
 ttg gca ggc aac ccc aag gcc acc cca ccc cag att gtc aac ggg gac 306  
 Leu Ala Gly Asn Pro Lys Ala Thr Pro Pro Gln Ile Val Asn Gly Asp  
 55 60 65  
 cag tac tgt ggg gac tat gag ctc ttc gtg gag gct gtg gaa caa aac 354  
 Gln Tyr Cys Gly Asp Tyr Glu Leu Phe Val Glu Ala Val Glu Gln Asn  
 70 75 80  
 acg ctg cag gag ttc ctg aag ctg gct tga gtcaagcctg tccagagttc 404  
 Thr Leu Gln Glu Phe Leu Lys Leu Ala  
 85 90  
 ccctgctgga ctccatcacc acactcccc cagccttcac ctggccatga aggacctttt 464  
 gaccaactcc ctgtcattcc taacctaac ttagagtccc tccccaatg caggccactt 524  
 ctctccctc ctctctaaat gtagtccct ctctccatc taaaggcaac attccttacc 584

09890688.092701

cattagtctc agaaaattgtc ttaagcaaca gccccaaatg ctggctgccc ccagccaagc 644  
 attggggccg ccatactgcc tggcactggc tgatgggcac ctctgttggt tccatcagcc 704  
 agagctctgc caaaggcccc gcagtccttc tcccaggagg accctagagg caattaaatg 764  
 atgtcctgtt ccattggc 782

<210> 96  
 <211> 93  
 <212> PRT  
 <213> Homo sapiens

<400> 96  
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 Ile Lys Ser Gln Ser Glu Val Thr Arg Ile Leu Asp Gly Lys Arg  
 20 25 30  
 Ile Gln Tyr Gln Leu Val Asp Ile Ser Gln Asp Asn Ala Leu Arg Asp  
 35 40 45  
 Glu Met Arg Ala Leu Ala Gly Asn Pro Lys Ala Thr Pro Pro Gln Ile  
 50 55 60  
 Val Asn Gly Asp Gln Tyr Cys Gly Asp Tyr Glu Leu Phe Val Glu Ala  
 65 70 75 80  
 Val Glu Gln Asn Thr Leu Gln Glu Phe Leu Lys Leu Ala  
 85 90

<210> 97  
 <211> 417  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (22)..(195)

<400> 97  
 ctagagcgcc gcgccccga g atg aag ccg gcg gtg gac gag atg ttc ccc 51  
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 1 5 10  
 gag ggc gcc ggg ccc tac gtg gac ctg gac gag gcg gga ggc agc acc 99  
 Glu Gly Ala Gly Pro Tyr Val Asp Leu Asp Glu Ala Gly Gly Ser Thr  
 15 20 25  
 ggg ctc ttg atg gac ttg gca gcc aat gaa aag gcc gtt cat gca gac 147  
 Gly Leu Leu Met Asp Leu Ala Ala Asn Glu Lys Ala Val His Ala Asp  
 30 35 40  
 ttt ttt aac gat ttt gaa gat ctt ttt gat gat gat gac atc cag tga 195  
 Phe Phe Asn Asp Phe Glu Asp Leu Phe Asp Asp Asp Asp Ile Gln  
 45 50 55  
 gatgccctct ggctgcaggc ggggccaaagc ccttggtaca gagccgcagt gtgagcctgc 255



gcaggacagt ttcaggtggt tttaaagaac acgtggaaat cccttgaatt taggacctgg 315  
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<210> 98  
 <211> 57  
 <212> PRT  
 <213> Homo sapiens

<400> 98  
 Met Lys Pro Ala Val Asp Glu Met Phe Pro Glu Gly Ala Gly Pro Tyr  
 1 5 10 15  
 Val Asp Leu Asp Glu Ala Gly Gly Ser Thr Gly Leu Leu Met Asp Leu  
 20 25 30  
 Ala Ala Asn Glu Lys Ala Val His Ala Asp Phe Phe Asn Asp Phe Glu  
 35 40 45  
 Asp Leu Phe Asp Asp Asp Asp Ile Gln  
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<210> 99  
 <211> 697  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (65)..(412)

<400> 99  
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 gaaa atg caa gct cag gcg ccg gtg gtc gtt gtg acc caa cct gga gtc 109  
 Met Gln Ala Gln Ala Pro Val Val Val Val Thr Gln Pro Gly Val  
 1 5 10 15  
 ggt ccc ggt ccg gcc ccc cag aac tcc aac tgg cag aca ggc atg tgt 157  
 Gly Pro Gly Pro Ala Pro Gln Asn Ser Asn Trp Gln Thr Gly Met Cys  
 20 25 30  
 gac tgt ttc agc gac tgc gga gtc tgt ctc tgt ggc aca ttt tgt ttc 205  
 Asp Cys Phe Ser Asp Cys Gly Val Cys Leu Cys Gly Thr Phe Cys Phe  
 35 40 45  
 ccg tgc ctt ggg tgt caa gtt gca gct gat atg aat gaa tgc tgt ctg 253  
 Pro Cys Leu Gly Cys Gln Val Ala Ala Asp Met Asn Glu Cys Cys Leu  
 50 55 60  
 tgt gga aca agc gtc gca atg agg act ctc tac agg acc cga tat ggc 301  
 Cys Gly Thr Ser Val Ala Met Arg Thr Leu Tyr Arg Thr Arg Tyr Gly  
 65 70 75  
 atc cct gga tct att tgt gat gac tat atg gca act ctt tgc tgt cct 349  
 Ile Pro Gly Ser Ile Cys Asp Asp Tyr Met Ala Thr Leu Cys Cys Pro

09890688-092701

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80              85              90              95
cat tgt act ctt tgc caa atc aag aga gat atc aac aga agg aga gcc 397
His Cys Thr Leu Cys Gln Ile Lys Arg Asp Ile Asn Arg Arg Arg Ala
              100              105              110

atg cgt act ttc taa aaactgatgg tgaaaagctc ttaccgaagc aacaaaattc 452
Met Arg Thr Phe
              115

agcagacacc tcttcagctt gagttcttca ccattctttg caactgaaat atgatggata 512

tgcttaagta caactgatgg catgaaaaaa atcaaatttt tgatttatta taaatgaatg 572

ttgtccctga acttagctaa atgggtgcaac ttagtttctc cttgctttca tattatcgaa 632

tttctctggct tataaacttt ttaaattaca ttgaaatat aaaccaaagc aaatatttta 692

ctgat 697

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<210> 100
<211> 115
<212> PRT
<213> Homo sapiens

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Pro Gly Pro Ala Pro Gln Asn Ser Asn Trp Gln Thr Gly Met Cys Asp
              20              25              30
Cys Phe Ser Asp Cys Gly Val Cys Leu Cys Gly Thr Phe Cys Phe Pro
              35              40              45
Cys Leu Gly Cys Gln Val Ala Ala Asp Met Asn Glu Cys Cys Leu Cys
              50              55              60
Gly Thr Ser Val Ala Met Arg Thr Leu Tyr Arg Thr Arg Tyr Gly Ile
              65              70              75              80
Pro Gly Ser Ile Cys Asp Asp Tyr Met Ala Thr Leu Cys Cys Pro His
              85              90              95
Cys Thr Leu Cys Gln Ile Lys Arg Asp Ile Asn Arg Arg Arg Ala Met
              100              105              110
Arg Thr Phe
              115

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<210> 101
<211> 1504
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (462)..(794)

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cgctgtaat	cccagcactt	tgggaggcca	aggcagggtg	atcacctgag	gtcggggagtt	180
caagaccagc	ctgaccaaca	tggagaaacc	ccatctctac	tagaaataca	aaattagcca	240
ggcatggtgg	tgcattgctg	taatcccagc	tactcgggag	gctgaagcag	gagaatcgct	300
taaatccggg	aggcggaggt	tgctgtgagc	cgagatcgcg	ccatttccag	cctggggcaac	360
aagagggaaa	ctccgtctca	aaaaaaaaaa	aaaaaaaaaga	agagaaaaga	aaacataagt	420
ttcagccagg	catgtgaagt	aagaactctg	ctagagagga	a atg gct gct tca tca		476
				Met Ala Ala Ser Ser		
				1	5	
tca tcc tcc tca gct ggt ggg gtc agt gga agt tct gtc act gga tct						524
Ser Ser Ser Ser Ala Gly Gly Val Ser Gly Ser Ser Val Thr Gly Ser						
	10			15	20	
ggt ttc agt gtc tca gac ctt gcc cca cca cgg aaa gcc ctt ttc acc						572
Gly Phe Ser Val Ser Asp Leu Ala Pro Pro Arg Lys Ala Leu Phe Thr						
	25			30	35	
tac ccc aaa gga gct gga gag atg tta gaa gat ggc tct gag aga ttc						620
Tyr Pro Lys Gly Ala Gly Glu Met Leu Glu Asp Gly Ser Glu Arg Phe						
	40			45	50	
ctc tgc gaa tct gtt ttt agc tat caa gtg gca tcc acg ctt aaa cag						668
Leu Cys Glu Ser Val Phe Ser Tyr Gln Val Ala Ser Thr Leu Lys Gln						
	55			60	65	
gtg aaa cat gat cag caa gtt gct cgg atg gaa aaa cta gct ggt ttg						716
Val Lys His Asp Gln Gln Val Ala Arg Met Glu Lys Leu Ala Gly Leu						
	70			75	80	85
gta gaa gag ctg gag gct gac gag tgg cgg ttt aag ccc atc gag cag						764
Val Glu Glu Leu Glu Ala Asp Glu Trp Arg Phe Lys Pro Ile Glu Gln						
	90			95	100	
ctg ctg gga ttc acc ccc tct tca ggt tga tactgcctgg atggtcacct						814
Leu Leu Gly Phe Thr Pro Ser Ser Gly						
	105			110		
ctggtgcgca gcaagtgcaa agccagtggg ggactttctc acagcttaca tagccatcca						874
gagatccaca gctacgtcac tgaattgtta atgcacattt gtacttggtt tctctgtatc						934
tattcacagg caacaaatac ttatatgtgt gatctttcag ggaatgtttt gtttatttgt						994
ttttaaaagt attgggaatc agattaagac aatcagtttc agagaaccag gaggttttggg						1054
gttaagagat actcaaaaaat tttcacaagc caagtagggc atatatcaga tttggccaac						1114
tgaatggcgt ctgtcctgtc atccatatgg tgccctggaaa tttttaccag tcaaggtcaa						1174

09890688.092701

ggtcagcatc tgtgggttaaa aatatagcat tctgacctaa aaaagttatt ttgcagatga 1234  
 atgtgttttc aactcaggac ctatccaaat gaggaatttt taaatattct ttttttttc 1294  
 ctatttttag acatcaattc tatagattct gactttttct aacctcttat agacatgcca 1354  
 aatgctggca aaaagaagtg ctttttggat atggcagcac ttgtaaaaat aaagcagtaa 1414  
 gcaaaatcct tttaaacaca gaaatcctga gttcttctca ttggtggact caagcaattc 1474  
 tgtagcaaat aaatcctttg aaagagctcc 1504

<210> 102  
 <211> 110  
 <212> PRT  
 <213> Homo sapiens

<400> 102  
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 1 5 10 15  
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 20 25 30  
 Lys Ala Leu Phe Thr Tyr Pro Lys Gly Ala Gly Glu Met Leu Glu Asp  
 35 40 45  
 Gly Ser Glu Arg Phe Leu Cys Glu Ser Val Phe Ser Tyr Gln Val Ala  
 50 55 60  
 Ser Thr Leu Lys Gln Val Lys His Asp Gln Gln Val Ala Arg Met Glu  
 65 70 75 80  
 Lys Leu Ala Gly Leu Val Glu Glu Leu Glu Ala Asp Glu Trp Arg Phe  
 85 90 95  
 Lys Pro Ile Glu Gln Leu Leu Gly Phe Thr Pro Ser Ser Gly  
 100 105 110

<210> 103  
 <211> 1046  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (124)..(525)

<400> 103  
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 ctgtttgtct gcttgcaactt ctggatcctg actgcccatt ggaggcatca gaccttcctt 120  
 ggg atg tgg tgt ggc tgt gat ggg aac ctg agt gtc cag acc tat tta 168  
 Met Trp Cys Gly Cys Asp Gly Asn Leu Ser Val Gln Thr Tyr Leu  
 1 5 10 15  
 ccg att gct cgt ggt ggg atc cct gcc ttc ctc ctc tgc ttg acc ccg 216  
 Pro Ile Ala Arg Gly Gly Ile Pro Ala Phe Leu Leu Cys Leu Thr Pro  
 20 25 30

09890688-092701

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ggt gtc cac gaa tgg tgt cct gac cct ctt ggg acg ctg aat gcc tgg 264
Gly Val His Glu Trp Cys Pro Asp Pro Leu Gly Thr Leu Asn Ala Trp
          35                40                45

agc tgt ctc gtg cct gct cgt ggt gcg atc ctt gtc ttc ctc cag tgc 312
Ser Cys Leu Val Pro Ala Arg Gly Ala Ile Leu Val Phe Leu Gln Cys
          50                55                60

tgg tcc cgg tcc gtc cat ggg cag agt cag gct gtt cat gag tgc tca 360
Trp Ser Arg Ser Val His Gly Gln Ser Gln Ala Val His Glu Cys Ser
          65                70                75

cct ggt aga ggg aag acc ctg aac gtc cag acc gtt ccc ctg acc ggc 408
Pro Gly Arg Gly Lys Thr Leu Asn Val Gln Thr Val Pro Leu Thr Gly
          80                85                90                95

cac gtg tgg act ctt ggt ggc tct gct gtc tca gcc cag cct ttc cgt 456
His Val Trp Thr Leu Gly Gly Ser Ala Val Ser Ala Gln Pro Phe Arg
          100                105                110

ggc ctg aca ctg att gtg tgt ctg agt ttt ctg aat gtc cct cac tgt 504
Gly Leu Thr Leu Ile Val Cys Leu Ser Phe Leu Asn Val Pro His Cys
          115                120                125

cac tgg cct gac tac cgc tag acccccggtg tccacgatcg ctgactgcag 555
His Trp Pro Asp Tyr Arg
          130

atgaagcttg cccgcgccca gtggctgagt gtctggagct gtctgctgac tgctggtggc 615

cggatccatg tctttctcct ggacttgatc ttgcctgttc atgggatgat gcagtctgtc 675

cacgagagga agtctctgcg tgacgagtgc ctgattgtct ggagctgtct gcagagtgcc 735

catgactggc tctgtcttca tcatgggacc tgggggtgtct ggagccatct cttgactgct 795

cccacgcaga tccatgatgg tttctggaag ccgaccacaga gtgcctctca gagtcttctg 855

agtgtccctc actgtccctg tccctggctaa ctctggatcc cctacgcttt cttgtcctgg 915

actcctgcaa tggtaacctg cttgtatttt catgtcttga cctgttcact tgagatgatg 975

atttgccatc agatgacett gatctttcat atattttgtt ttcttctaag agactatcag 1035

tggtgtcata g 1046

<210> 104
<211> 133
<212> PRT
<213> Homo sapiens

<400> 104
Met Trp Cys Gly Cys Asp Gly Asn Leu Ser Val Gln Thr Tyr Leu Pro
  1          5                10                15
Ile Ala Arg Gly Gly Ile Pro Ala Phe Leu Leu Cys Leu Thr Pro Gly

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[illegible]

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<210> 105
<211> 341
<212> DNA
<213> Homo sapiens
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<220>  
<221> CDS  
<222> (55)..(261)
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<220>  
<221> residue  
<222> (9)  
<223> Xaa = selenocysteine
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[illegible]

<210> 106  
 <211> 68  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> residue  
 <222> (9)  
 <223> Xaa = selenocysteine

<400> 106  
 Met Cys Tyr Asp Leu Gly Thr Asn Xaa Ala Thr Ser Val Ala Leu Arg  
 1 5 10 15  
 Ala Val Arg Thr Leu Gln Ala Gly Gln Val Pro Gly Arg Pro Gly Leu  
 20 25 30  
 Ala Tyr Ala Pro Leu Cys Pro Leu Ala Phe Lys Gly Phe Phe Pro Asn  
 35 40 45  
 Leu Arg Pro Ser Ala Thr Cys Arg Phe Arg Arg Glu Pro Ala Ala Ser  
 50 55 60  
 Phe Glu Pro Lys  
 65

<210> 107  
 <211> 1684  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (13)..(1011)

<400> 107  
 ttctctcgtg ca atg gcg tcc ggg ctg gta aga ttg ctg cag cag gga cat 51  
 Met Ala Ser Gly Leu Val Arg Leu Leu Gln Gln Gly His  
 1 5 10  
 cgc tgc ctc ctg gct cca gtc gcc ccc aag ctg gtc cct ccg gtt cgg 99  
 Arg Cys Leu Leu Ala Pro Val Ala Pro Lys Leu Val Pro Pro Val Arg  
 15 20 25  
 gga gtg aag aag gga ttc cgc gcc gcc ttc cgc ttc cag aag gag tta 147  
 Gly Val Lys Lys Gly Phe Arg Ala Ala Phe Arg Phe Gln Lys Glu Leu  
 30 35 40 45  
 gag cgg cag cgc ctt ctg cgg tgc ccg ccg ccg ccc gtg cgc cgt tca 195  
 Glu Arg Gln Arg Leu Leu Arg Cys Pro Pro Pro Pro Val Arg Arg Ser  
 50 55 60  
 gag aag ccg aac tgg gat tac cat gca gaa ata caa gct ttt gga cat 243  
 Glu Lys Pro Asn Trp Asp Tyr His Ala Glu Ile Gln Ala Phe Gly His  
 65 70 75  
 cgg tta cag gaa aac ttt tcc tta gat ctt ctc aaa act gca ttt gtt 291  
 Arg Leu Gln Glu Asn Phe Ser Leu Asp Leu Leu Lys Thr Ala Phe Val

0950688-02701

80	85	90	
aat agc tgc tat att aaa agt gag gag gcc aaa cgc caa caa ctt ggg Asn Ser Cys Tyr Ile Lys Ser Glu Glu Ala Lys Arg Gln Gln Leu Gly 95 100 105			339
ata gag aaa gaa gct gtt ctt ctg aat ctt aaa agt aat caa gaa cta Ile Glu Lys Glu Ala Val Leu Leu Asn Leu Lys Ser Asn Gln Glu Leu 110 115 120 125			387
tcc gaa caa ggg aca tct ttt tca cag act tgc ctt aca cag ttt ctt Ser Glu Gln Gly Thr Ser Phe Ser Gln Thr Cys Leu Thr Gln Phe Leu 130 135 140			435
gaa gac gag tac cca gac atg ccc act gaa ggc ata aaa aat ctt gtt Glu Asp Glu Tyr Pro Asp Met Pro Thr Glu Gly Ile Lys Asn Leu Val 145 150 155			483
gac ttt ctc act ggt gag gaa gtc gtg tgt cac gtg gct aga aac ttg Asp Phe Leu Thr Gly Glu Glu Val Val Cys His Val Ala Arg Asn Leu 160 165 170			531
gct gtg gag cag tta aca ctg agt gaa gaa ttc cca gtg ccc cca gct Ala Val Glu Gln Leu Thr Leu Ser Glu Glu Phe Pro Val Pro Pro Ala 175 180 185			579
gtg tta cag cag act ttc ttt gca gtt att gga gcc ctg tta cag agc Val Leu Gln Gln Thr Phe Phe Ala Val Ile Gly Ala Leu Leu Gln Ser 190 195 200 205			627
agt gga cct gag agg act gca ctt ttc atc agg gac ttc tta att act Ser Gly Pro Glu Arg Thr Ala Leu Phe Ile Arg Asp Phe Leu Ile Thr 210 215 220			675
caa atg act gga aaa gag ctc ttt gag atg tgg aag ata ata aat ccc Gln Met Thr Gly Lys Glu Leu Phe Glu Met Trp Lys Ile Ile Asn Pro 225 230 235			723
atg ggg cta ttg gta gaa gaa ctg aag aaa agg aat gtt tca gct cct Met Gly Leu Leu Val Glu Glu Leu Lys Lys Arg Asn Val Ser Ala Pro 240 245 250			771
gaa tca aga ctt act agg cag tct ggt ggc acc aca gct ttg cct ttg Glu Ser Arg Leu Thr Arg Gln Ser Gly Gly Thr Thr Ala Leu Pro Leu 255 260 265			819
tat ttt gtt ggc tta tac tgt gat aaa aag ttg att gca gaa gga cct Tyr Phe Val Gly Leu Tyr Cys Asp Lys Lys Leu Ile Ala Glu Gly Pro 270 275 280 285			867
ggg gaa aca gta ttg gtt gca gaa gaa gag gct gct cga gtg gcc ctt Gly Glu Thr Val Leu Val Ala Glu Glu Ala Ala Arg Val Ala Leu 290 295 300			915
aga aaa ctt tat gga ttc aca gaa aat aga cgg ccg tgg aac tat tcc Arg Lys Leu Tyr Gly Phe Thr Glu Asn Arg Arg Pro Trp Asn Tyr Ser 305 310 315			963



09890688.092701

aag ccc aaa gaa acc ttg aga gca gaa aag agc atc act gcc agc tag 1011  
 Lys Pro Lys Glu Thr Leu Arg Ala Glu Lys Ser Ile Thr Ala Ser  
 320 325 330

ccgccatgga tgcagcagcc tgaaacttga gagcgaaagt gagataaatg tcaaaggtgt 1071  
 ttcaagccag acattttcac aattgtgaag aaatagatgt tttgtttctg ttttttactg 1131  
 tgttcccaaa attaaataaa tgtaaaccaa gtcacagtgt ttttggtttt gtttttctga 1191  
 aatcttggtt tgatcaaatac tttttttttt tctcttgaga tggagtctta ctctgtcgcc 1251  
 caggctggac tgcagtgggtg cgatctcggc tcaactgcaac ctccacctca caggttcaag 1311  
 cgattctcgt ggctcagcct ccctagtagc tgggattaca ggcacacacc accatacctg 1371  
 gctaattttt gtatttttgg tagacatggg gtttcaccaa gttggctagg ctagtcttga 1431  
 actcctgacc tcaggtgatc caccgcctt ggcctcccaa agtgctggga ttacaggtgt 1491  
 gagccactat acccgaccag atcaaactct tttttgacat ttttgcaaaa aaattttcct 1551  
 aatgttcttg atttaattgt atagaatttg tataattagg tgtattttat ttgcgtctag 1611  
 ctttgaggta tcataattta tgtatcttat gtgaattttt tgctgtaata ccaataaagt 1671  
 tttttttctc cac 1684

<210> 108  
 <211> 332  
 <212> PRT  
 <213> Homo sapiens

<400> 108  
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 Leu Ala Pro Val Ala Pro Lys Leu Val Pro Pro Val Arg Gly Val Lys  
 20 25 30  
 Lys Gly Phe Arg Ala Ala Phe Arg Phe Gln Lys Glu Leu Glu Arg Gln  
 35 40 45  
 Arg Leu Leu Arg Cys Pro Pro Pro Val Arg Arg Ser Glu Lys Pro  
 50 55 60  
 Asn Trp Asp Tyr His Ala Glu Ile Gln Ala Phe Gly His Arg Leu Gln  
 65 70 75 80  
 Glu Asn Phe Ser Leu Asp Leu Leu Lys Thr Ala Phe Val Asn Ser Cys  
 85 90 95  
 Tyr Ile Lys Ser Glu Glu Ala Lys Arg Gln Gln Leu Gly Ile Glu Lys  
 100 105 110  
 Glu Ala Val Leu Leu Asn Leu Lys Ser Asn Gln Glu Leu Ser Glu Gln  
 115 120 125  
 Gly Thr Ser Phe Ser Gln Thr Cys Leu Thr Gln Phe Leu Glu Asp Glu  
 130 135 140  
 Tyr Pro Asp Met Pro Thr Glu Gly Ile Lys Asn Leu Val Asp Phe Leu  
 145 150 155 160  
 Thr Gly Glu Glu Val Val Cys His Val Ala Arg Asn Leu Ala Val Glu

					165					170					175	
Gln	Leu	Thr	Leu	Ser	Glu	Glu	Phe	Pro	Val	Pro	Pro	Ala	Val	Leu	Gln	
			180					185					190			
Gln	Thr	Phe	Phe	Ala	Val	Ile	Gly	Ala	Leu	Leu	Gln	Ser	Ser	Gly	Pro	
		195					200					205				
Glu	Arg	Thr	Ala	Leu	Phe	Ile	Arg	Asp	Phe	Leu	Ile	Thr	Gln	Met	Thr	
	210					215					220					
Gly	Lys	Glu	Leu	Phe	Glu	Met	Trp	Lys	Ile	Ile	Asn	Pro	Met	Gly	Leu	
225					230					235					240	
Leu	Val	Glu	Glu	Leu	Lys	Lys	Arg	Asn	Val	Ser	Ala	Pro	Glu	Ser	Arg	
			245						250					255		
Leu	Thr	Arg	Gln	Ser	Gly	Gly	Thr	Thr	Ala	Leu	Pro	Leu	Tyr	Phe	Val	
			260					265					270			
Gly	Leu	Tyr	Cys	Asp	Lys	Lys	Leu	Ile	Ala	Glu	Gly	Pro	Gly	Glu	Thr	
		275					280					285				
Val	Leu	Val	Ala	Glu	Glu	Glu	Ala	Ala	Arg	Val	Ala	Leu	Arg	Lys	Leu	
	290					295					300					
Tyr	Gly	Phe	Thr	Glu	Asn	Arg	Arg	Pro	Trp	Asn	Tyr	Ser	Lys	Pro	Lys	
305					310					315					320	
Glu	Thr	Leu	Arg	Ala	Glu	Lys	Ser	Ile	Thr	Ala	Ser					
			325						330							

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<220>  
<221> CDS  
<222> (81) .. (560)
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gccccggacc aggtgcctcc atg gca ggc tct gaa gag ctg ggg ctc cgg gaa 113  
Met Ala Gly Ser Glu Glu Leu Gly Leu Arg Glu  
1 5 10

ggg tct cct gtt cca act cca cct aga agc cct gcc caa gaa gag cca 209  
Gly Ser Pro Val Pro Thr Pro Pro Arg Ser Pro Ala Gln Glu Glu Pro  
30 35 40

cga gga gca gcc ccc tct gag tcc cct cgg cct tgc tct ctg ccc atc 305  
Arg Gly Ala Ala Pro Ser Glu Ser Pro Arg Pro Cys Ser Leu Pro Ile  
60 65 70 75

cgc ccc tgc tat ggt tta gag cct ggc cca gct act cca gac ttc tat 353  
Arg Pro Cys Tyr Gly Leu Glu Pro Gly Pro Ala Thr Pro Asp Phe Tyr

	80		85		90	
	gct ttg gtg gcc cag cgg ctg gaa cag ctg gtc caa gag cag ctg aaa					401
	Ala Leu Val Ala Gln Arg Leu Glu Gln Leu Val Gln Glu Gln Leu Lys					
	95		100		105	
	tct ccg ccc agc cca gaa tta cag ggt ccc cca tcg aca gag aag gaa					449
	Ser Pro Pro Ser Pro Glu Leu Gln Gly Pro Pro Ser Thr Glu Lys Glu					
	110		115		120	
	gcc ata ctg cgg agg ctg gtg gcc ctg ctg gag gag gag gca gaa gtc					497
	Ala Ile Leu Arg Arg Leu Val Ala Leu Leu Glu Glu Glu Ala Glu Val					
	125		130		135	
	att aac cag aag gag ggc atc ctg gct gtt tca ccc gtg gac ttg aac					545
	Ile Asn Gln Lys Glu Gly Ile Leu Ala Val Ser Pro Val Asp Leu Asn					
	140		145		150	155
	ttg cca ttg gac tga gctctttctc agaagctgct acaagatgac acctcatgct					600
	Leu Pro Leu Asp					
	cctgccctct tcgtgtgctt ttccaagtct tectattcca ctcagggctg tggggtggtg					660
	gttgccctac ctgtttttgc caaaaataaa ttgtttaaaa cttttcttat taaaaacgtt					720
	acaaagt					727
	<210> 110					
	<211> 159					
	<212> PRT					
	<213> Homo sapiens					
	<400> 110					
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	1 5 10 15					
	Leu Ala Ala Phe Leu Arg Arg Gly Glu Ala Ala Gly Ser Pro Val Pro					
	20 25 30					
	Thr Pro Pro Arg Ser Pro Ala Gln Glu Glu Pro Thr Asp Phe Leu Ser					
	35 40 45					
	Arg Leu Arg Arg Cys Leu Pro Cys Ser Leu Gly Arg Gly Ala Ala Pro					
	50 55 60					
	Ser Glu Ser Pro Arg Pro Cys Ser Leu Pro Ile Arg Pro Cys Tyr Gly					
	65 70 75 80					
	Leu Glu Pro Gly Pro Ala Thr Pro Asp Phe Tyr Ala Leu Val Ala Gln					
	85 90 95					
	Arg Leu Glu Gln Leu Val Gln Glu Gln Leu Lys Ser Pro Pro Ser Pro					
	100 105 110					
	Glu Leu Gln Gly Pro Pro Ser Thr Glu Lys Glu Ala Ile Leu Arg Arg					
	115 120 125					
	Leu Val Ala Leu Leu Glu Glu Glu Ala Glu Val Ile Asn Gln Lys Glu					
	130 135 140					
	Gly Ile Leu Ala Val Ser Pro Val Asp Leu Asn Leu Pro Leu Asp					
	145 150 155					

<210> 111  
 <211> 1354  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (133)..(870)

<400> 111  
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 accctccggg ccttctgccc ctgatcgctt ggttttcctt gcagtcgcct gctgctgctg 120  
 tcgggaggaa ag atg aat ggg agg gct gat ttt cga gag ccg aat gca gag 171  
                   Met Asn Gly Arg Ala Asp Phe Arg Glu Pro Asn Ala Glu  
                   1                  5                  10  
 gtt cca aga cca att ccc cac ata ggg cct gat tac att cca aca gag 219  
 Val Pro Arg Pro Ile Pro His Ile Gly Pro Asp Tyr Ile Pro Thr Glu  
                   15                  20                  25  
 gaa gaa agg aga gtc ttc gca gaa tgc aat gat gaa agc ttc tgg ttc 267  
 Glu Glu Arg Arg Val Phe Ala Glu Cys Asn Asp Glu Ser Phe Trp Phe  
                   30                  35                  40                  45  
 aga tct gtg cct ttg gct gca aca agt atg ttg att act caa gga tta 315  
 Arg Ser Val Pro Leu Ala Ala Thr Ser Met Leu Ile Thr Gln Gly Leu  
                   50                  55                  60  
 att agt aaa gga ata ctt tca agt cat ccc aaa tat ggt tcc atc cct 363  
 Ile Ser Lys Gly Ile Leu Ser Ser His Pro Lys Tyr Gly Ser Ile Pro  
                   65                  70                  75  
 aaa ctt ata ctt gct tgt atc atg gga tac ttt gct gga aaa ctt tct 411  
 Lys Leu Ile Leu Ala Cys Ile Met Gly Tyr Phe Ala Gly Lys Leu Ser  
                   80                  85                  90  
 tat gtg aaa act tgc caa gag aaa ttc aag aaa ctt gaa aat tcc ccc 459  
 Tyr Val Lys Thr Cys Gln Glu Lys Phe Lys Lys Leu Glu Asn Ser Pro  
                   95                  100                  105  
 ctt gga gaa gct tta cga tca gga caa gca cga cga tct tca cca cct 507  
 Leu Gly Glu Ala Leu Arg Ser Gly Gln Ala Arg Arg Ser Ser Pro Pro  
                   110                  115                  120                  125  
 ggg cac tat tat caa aag tca aaa tat gac tca agt gtg agt ggt caa 555  
 Gly His Tyr Tyr Gln Lys Ser Lys Tyr Asp Ser Ser Val Ser Gly Gln  
                   130                  135                  140  
 tca tct ttt gtg aca tcc cca gca gca gac aac ata gaa atg ctt cct 603  
 Ser Ser Phe Val Thr Ser Pro Ala Ala Asp Asn Ile Glu Met Leu Pro  
                   145                  150                  155  
 cat tat gag cca att cca ttc agt tct tct atg aat gaa tct gct ccc 651  
 His Tyr Glu Pro Ile Pro Phe Ser Ser Ser Met Asn Glu Ser Ala Pro  
                   160                  165                  170

00330688-092701

act ggt att act gat cat att gtc caa gga cct gat ccc aac ctt gaa 699  
 Thr Gly Ile Thr Asp His Ile Val Gln Gly Pro Asp Pro Asn Leu Glu  
 175 180 185

gaa agt cct aaa aga aaa aat att aca tat gag gaa tta agg aat aag 747  
 Glu Ser Pro Lys Arg Lys Asn Ile Thr Tyr Glu Glu Leu Arg Asn Lys  
 190 195 200 205

aac aga gag tca tat gaa gta tct tta aca caa aag act gac ccc tca 795  
 Asn Arg Glu Ser Tyr Glu Val Ser Leu Thr Gln Lys Thr Asp Pro Ser  
 210 215 220

gtc agg cct atg cat gaa aga gtg cca aaa aaa gaa gtc aaa gta aac 843  
 Val Arg Pro Met His Glu Arg Val Pro Lys Lys Glu Val Lys Val Asn  
 225 230 235

aag tat gga gat act tgg gat gag tga aaaattacat cattggacat 890  
 Lys Tyr Gly Asp Thr Trp Asp Glu  
 240 245

gaaggagttt caacatccag cttcatctag gtggatcatga ttacctgcat gctttgagct 950

cagcagcagt cttcataaac acatttaaaa caagatcctg gggttttgtg gtttgacttc 1010

tatggtgttt taaaaaaaca cagattttta gtgttaatat tgtgtaaatg tactcacctt 1070

agggattcat ttgaatgatg gtattatacc atgattgtat acagtttgtg aaattgttgc 1130

aagggcaaag ataactctta aaaaaccgtc gagattacaa tgctctagaa tcagcatata 1190

agaaaataaa tgatatctgc atgttgaatt ggggtggatg gggggagcaa gcataatttt 1250

taagtgtgaa gctttgcatc aagaaattat taaaaagctt tttttctcca gtattttctg 1310

tattatctta atgtttatgg caaataaaat gtaaaggaac atgc 1354

<210> 112  
 <211> 245  
 <212> PRT  
 <213> Homo sapiens

<400> 112  
 Met Asn Gly Arg Ala Asp Phe Arg Glu Pro Asn Ala Glu Val Pro Arg  
 1 5 10 15  
 Pro Ile Pro His Ile Gly Pro Asp Tyr Ile Pro Thr Glu Glu Glu Arg  
 20 25 30  
 Arg Val Phe Ala Glu Cys Asn Asp Glu Ser Phe Trp Phe Arg Ser Val  
 35 40 45  
 Pro Leu Ala Ala Thr Ser Met Leu Ile Thr Gln Gly Leu Ile Ser Lys  
 50 55 60  
 Gly Ile Leu Ser Ser His Pro Lys Tyr Gly Ser Ile Pro Lys Leu Ile  
 65 70 75 80  
 Leu Ala Cys Ile Met Gly Tyr Phe Ala Gly Lys Leu Ser Tyr Val Lys  
 85 90 95  
 Thr Cys Gln Glu Lys Phe Lys Lys Leu Glu Asn Ser Pro Leu Gly Glu

[illegible]

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<210> 113
<211> 653
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> (170)..(502)
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<400> 113
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aaggcgggtc gttccccccg gacagcccta cgccggcaaa ggtctcgag atg  cag  gcg 178
                                     Met  Gln  Ala
                                     1

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gcc cta gag gtc acc gct cgc tac tgt ggc cgg gag ctg gag cag tat 226  
Ala Leu Glu Val Thr Ala Arg Tyr Cys Gly Arg Glu Leu Glu Gln Tyr  
5 10 15

ggc cag tgt gtg gcg gcc aag ccg gaa tcc tgg cag cgg gac tgt cac 274  
Gly Gln Cys Val Ala Ala Lys Pro Glu Ser Trp Gln Arg Asp Cys His  
20 25 30 35

tac ctt aag atg agc att gcc cag tgc aca tcc tcc cac cca atc atc 322  
 Tyr Leu Lys Met Ser Ile Ala Gln Cys Thr Ser Ser His Pro Ile Ile  
 40 45 50

cgc cag atc cgc cag gcc tgt gct cag cct ttt gag gcc ttc gag gag 370  
 Arg Gln Ile Arg Gln Ala Cys Ala Gln Pro Phe Glu Ala Phe Glu Glu  
 55 60 65

tgt ctt cga cag aac gag gca gct gtg ggc aac tgt gca gag cat atg 418  
Cys Leu Arg Gln Asn Glu Ala Ala Val Gly Asn Cys Ala Glu His Met

09890688.092701

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              70              75              80
cgc cgc ttc ctg cag tgc gct gag cag gtg cag ccg cca cgc tca cct 466
Arg Arg Phe Leu Gln Cys Ala Glu Gln Val Gln Pro Pro Arg Ser Pro
      85              90              95

gca act gtg gag gca cag cca ctt cct gcc tcc tga ggactcctct 512
Ala Thr Val Glu Ala Gln Pro Leu Pro Ala Ser
100              105              110

gacggcagga aaactggaca tgaatgactg cccccccgcc cctcccctgc agagtggcca 572

gatggagtcc tgagccctgg acatggggccc ggctttcctg gatatcagga cttccaataa 632

ataaagactc tgtatactgg g 653

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<210> 114  
 <211> 110  
 <212> PRT  
 <213> Homo sapiens

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<400> 114
Met Gln Ala Ala Leu Glu Val Thr Ala Arg Tyr Cys Gly Arg Glu Leu
 1              5              10              15
Glu Gln Tyr Gly Gln Cys Val Ala Ala Lys Pro Glu Ser Trp Gln Arg
      20              25              30
Asp Cys His Tyr Leu Lys Met Ser Ile Ala Gln Cys Thr Ser Ser His
      35              40              45
Pro Ile Ile Arg Gln Ile Arg Gln Ala Cys Ala Gln Pro Phe Glu Ala
      50              55              60
Phe Glu Glu Cys Leu Arg Gln Asn Glu Ala Ala Val Gly Asn Cys Ala
      65              70              75              80
Glu His Met Arg Arg Phe Leu Gln Cys Ala Glu Gln Val Gln Pro Pro
      85              90              95
Arg Ser Pro Ala Thr Val Glu Ala Gln Pro Leu Pro Ala Ser
      100              105              110

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<210> 115  
 <211> 643  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (40)..(411)

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<400> 115
gcggaagtac ggaccgtgaa ctggagtgga atcgcgact atg gga gct ccg ggg 54
              Met Gly Ala Pro Gly
              1              5

gga aag atc aac cgg ccc cga acg gag ctg aag aag aag ctg ttc aaa 102
Gly Lys Ile Asn Arg Pro Arg Thr Glu Leu Lys Lys Lys Leu Phe Lys
      10              15              20

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09890688-092704

cgc cgg cgg gtg ttg aat cgg gag cgg cgt ctg agg cac cgg gtg gtc 150  
 Arg Arg Arg Val Leu Asn Arg Glu Arg Arg Leu Arg His Arg Val Val  
                   25                                  30                                  35

ggg gct gtg ata gac caa ggg ctg atc acg cgg cac cac ctc aag aag 198  
 Gly Ala Val Ile Asp Gln Gly Leu Ile Thr Arg His His Leu Lys Lys  
                   40                                  45                                  50

cgg gcg tcc agt gca cgt gcc aac att aca ctg tca ggg aag aag cgc 246  
 Arg Ala Ser Ser Ala Arg Ala Asn Ile Thr Leu Ser Gly Lys Lys Arg  
                   55                                  60                                  65

aga aaa ctc ctc cag cag atc cgg ctt gcc cag aaa gag aag aca gcc 294  
 Arg Lys Leu Leu Gln Gln Ile Arg Leu Ala Gln Lys Glu Lys Thr Ala  
                   70                                  75                                  80                                  85

atg gaa gtg gaa gcc cct tca aag cca gcc agg act agt gaa cca cag 342  
 Met Glu Val Glu Ala Pro Ser Lys Pro Ala Arg Thr Ser Glu Pro Gln  
                                   90                                  95                                  100

ctc aaa agg caa aag aag aca aaa gcc ccc cag gat gta gaa atg aag 390  
 Leu Lys Arg Gln Lys Lys Thr Lys Ala Pro Gln Asp Val Glu Met Lys  
                   105                                  110                                  115

gac ctt gaa gat gag agc taa acctcttcca ctagaagatt ctcaactgga 441  
 Asp Leu Glu Asp Glu Ser  
                   120

gccagccttc agactcagtg gttgtttcag aggactttga caaaagcaag gccccttttc 501

actctccaga ttctctccta cctaattggcc tactgacctc ccctagaggg atgtcttttg 561

gagggaagaa ggtacagaag aaagattgga gaagggtctc tctagcagtc aactccattt 621

gtaataaagc cctagcactc tg 643

<210> 116  
 <211> 123  
 <212> PRT  
 <213> Homo sapiens

<400> 116  
 Met Gly Ala Pro Gly Gly Lys Ile Asn Arg Pro Arg Thr Glu Leu Lys  
   1                                  5                                  10                                  15  
 Lys Lys Leu Phe Lys Arg Arg Arg Val Leu Asn Arg Glu Arg Arg Leu  
                   20                                  25                                  30  
 Arg His Arg Val Val Gly Ala Val Ile Asp Gln Gly Leu Ile Thr Arg  
                   35                                  40                                  45  
 His His Leu Lys Lys Arg Ala Ser Ser Ala Arg Ala Asn Ile Thr Leu  
                   50                                  55                                  60  
 Ser Gly Lys Lys Arg Arg Lys Leu Leu Gln Gln Ile Arg Leu Ala Gln  
                   65                                  70                                  75                                  80  
 Lys Glu Lys Thr Ala Met Glu Val Glu Ala Pro Ser Lys Pro Ala Arg  
                                   85                                  90                                  95  
 Thr Ser Glu Pro Gln Leu Lys Arg Gln Lys Lys Thr Lys Ala Pro Gln  
                   100                                  105                                  110



Asp Val Glu Met Lys Asp Leu Glu Asp Glu Ser  
115 120

<210> 117  
<211> 1293  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (306)..(1019)

<400> 117  
gtaggctga gcctcttgct tgctgtgact ggtggagctg ccgcgctgtc cgcgttatct 60  
cctcccgggtg agaacgaacc gcagtgtcca ccggcgagga gccagccctg tcccggtcag 120  
agaaagacga cgaggatacc tgggagcggg cgggcgccgg gctgggccgc gccgggtgcgg 180  
gctggcgact ctgctcctcc gcttgctgct gtctctggga actgggtgcc agcgtgagg 240  
ggcttccagc ggacagggac ccccttcccc ggtccccctg cccaccctgc cggggagggc 300  
ggaag atg ccg gtg aag aag aag aga aaa tcc cct ggg gtg gca gca gca 350  
Met Pro Val Lys Lys Lys Arg Lys Ser Pro Gly Val Ala Ala Ala  
1 5 10 15  
gta gcg gaa gac gga ggc ctc aaa aag tgt aaa atc tcc agc tat tgc 398  
Val Ala Glu Asp Gly Gly Leu Lys Lys Cys Lys Ile Ser Ser Tyr Cys  
20 25 30  
aga tcc caa ccc cct gct aga cta ata agt gga gag gaa cat ttt tca 446  
Arg Ser Gln Pro Pro Ala Arg Leu Ile Ser Gly Glu Glu His Phe Ser  
35 40 45  
agc aag aag tgc ctg gct tgg ttt tat gaa tat gca ggt cct gat gaa 494  
Ser Lys Lys Cys Leu Ala Trp Phe Tyr Glu Tyr Ala Gly Pro Asp Glu  
50 55 60  
gtt gta ggg cca gaa gga atg gaa aaa ttt tgt gaa gac att ggt gtt 542  
Val Val Gly Pro Glu Gly Met Glu Lys Phe Cys Glu Asp Ile Gly Val  
65 70 75  
gaa cct gaa aat att att atg tta gtt tta gcg tgg aaa ttg gag gct 590  
Glu Pro Glu Asn Ile Ile Met Leu Val Leu Ala Trp Lys Leu Glu Ala  
80 85 90 95  
gaa agc atg gga ttt ttt acc aag gaa gaa tgg tta aag gga atg act 638  
Glu Ser Met Gly Phe Phe Thr Lys Glu Glu Trp Leu Lys Gly Met Thr  
100 105 110  
tca tta cag tgt gac tgc aca gaa aag tta caa aac aaa ttt gac ttt 686  
Ser Leu Gln Cys Asp Cys Thr Glu Lys Leu Gln Asn Lys Phe Asp Phe  
115 120 125  
ttg cgc tca cag ttg aat gat att tcg tca ttt aag aat atc tac aga 734

09390688-092701

Leu Arg Ser Gln Leu Asn Asp Ile Ser Ser Phe Lys Asn Ile Tyr Arg  
130 135 140

tat gcc ttt gat ttt gca agg gat aaa gat cag aga agc ctt gat att 782  
Tyr Ala Phe Asp Phe Ala Arg Asp Lys Asp Gln Arg Ser Leu Asp Ile  
145 150 155

gat act gct aaa tct atg tta gct ctt ctg ctt ggg agg aca tgg cca 830  
Asp Thr Ala Lys Ser Met Leu Ala Leu Leu Leu Gly Arg Thr Trp Pro  
160 165 170 175

ctg ttt tca gta ttt tac cag tac ctg gag caa tca aag tat cgt gtt 878  
Leu Phe Ser Val Phe Tyr Gln Tyr Leu Glu Gln Ser Lys Tyr Arg Val  
180 185 190

atg aac aaa gat caa tgg tac aat gta tta gaa ttc agc aga aca gtc 926  
Met Asn Lys Asp Gln Trp Tyr Asn Val Leu Glu Phe Ser Arg Thr Val  
195 200 205

cat gct gat ctt agt aac tat gat gaa gat ggt gct tgg cct gtt ctt 974  
His Ala Asp Leu Ser Asn Tyr Asp Glu Asp Gly Ala Trp Pro Val Leu  
210 215 220

ctt gat gaa ttt gtt gag tgg caa aaa gtc cgt cag aca tca tag 1019  
Leu Asp Glu Phe Val Glu Trp Gln Lys Val Arg Gln Thr Ser  
225 230 235

caagaactat gtgaagaaaa tgcaaacctt tcaattccca cgtgtataca agctaattgtg 1079

atgaggggga aaaaaatcca acgggtgcat ttctattcat atgaaagact tctcatagta 1139

cttttttttc ctttttttaa aggaggtttt tcttgttaca tgtgatgggc attgagccac 1199

acctcttctt agactgaata ttgaagtttt tgttttgagt tatgtttata acatttattt 1259

cagaacaata aagattcaga tttgtgacaa aggc 1293

<210> 118  
<211> 237  
<212> PRT  
<213> Homo sapiens

<400> 118  
Met Pro Val Lys Lys Lys Arg Lys Ser Pro Gly Val Ala Ala Ala Val  
1 5 10 15  
Ala Glu Asp Gly Gly Leu Lys Lys Cys Lys Ile Ser Ser Tyr Cys Arg  
20 25 30  
Ser Gln Pro Pro Ala Arg Leu Ile Ser Gly Glu Glu His Phe Ser Ser  
35 40 45  
Lys Lys Cys Leu Ala Trp Phe Tyr Glu Tyr Ala Gly Pro Asp Glu Val  
50 55 60  
Val Gly Pro Glu Gly Met Glu Lys Phe Cys Glu Asp Ile Gly Val Glu  
65 70 75 80  
Pro Glu Asn Ile Ile Met Leu Val Leu Ala Trp Lys Leu Glu Ala Glu  
85 90 95  
Ser Met Gly Phe Phe Thr Lys Glu Glu Trp Leu Lys Gly Met Thr Ser

				100				105				110			
Leu	Gln	Cys	Asp	Cys	Thr	Glu	Lys	Leu	Gln	Asn	Lys	Phe	Asp	Phe	Leu
115				120				125							
Arg	Ser	Gln	Leu	Asn	Asp	Ile	Ser	Ser	Phe	Lys	Asn	Ile	Tyr	Arg	Tyr
130				135				140							
Ala	Phe	Asp	Phe	Ala	Arg	Asp	Lys	Asp	Gln	Arg	Ser	Leu	Asp	Ile	Asp
145				150				155				160			
Thr	Ala	Lys	Ser	Met	Leu	Ala	Leu	Leu	Leu	Gly	Arg	Thr	Trp	Pro	Leu
165				170				175							
Phe	Ser	Val	Phe	Tyr	Gln	Tyr	Leu	Glu	Gln	Ser	Lys	Tyr	Arg	Val	Met
180				185				190							
Asn	Lys	Asp	Gln	Trp	Tyr	Asn	Val	Leu	Glu	Phe	Ser	Arg	Thr	Val	His
195				200				205							
Ala	Asp	Leu	Ser	Asn	Tyr	Asp	Glu	Asp	Gly	Ala	Trp	Pro	Val	Leu	Leu
210				215				220							
Asp	Glu	Phe	Val	Glu	Trp	Gln	Lys	Val	Arg	Gln	Thr	Ser			
225				230				235							

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<220>
<221> CDS
<222> (148)..(471)
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tcc tac ccg gtt gtg aag agg agg gag ggg ccc gct ggg cac agc aag 222  
Ser Tyr Pro Val Val Lys Arg Arg Glu Gly Pro Ala Gly His Ser Lys  
10 15 20 25

gag gaa gcg gag ctg gag ctg ctg agg cag ttt gac ctg gcc tgg cag 318  
Glu Glu Ala Glu Leu Glu Leu Leu Arg Gln Phe Asp Leu Ala Trp Gln  
45 50 55

aag cag atg ggc ttg gag cct ccc cca gag gtg tgg cag gtg ctg aag 414  
Lys Gln Met Gly Leu Glu Pro Pro Pro Glu Val Trp Gln Val Leu Lys  
75 80 85

09890688.092701

acc cac ccc gga gac ccc cgc ttc cag tgc agt ctc tgg cat ctc tat 462  
 Thr His Pro Gly Asp Pro Arg Phe Gln Cys Ser Leu Trp His Leu Tyr  
 90 95 100 105

ccc cta tga ggcaccacgt aagacctcct gcccttagct ctcttgctca 511  
 Pro Leu

ccaccaaga acctcaggac agaagcgaga gccattgct cctgctcagc tcagcccggc 571  
 tgcggaggaa cccttggcag gcagaacctg gaggtgtcag aggtcaact cctccatcta 631  
 accagcaggc tcccagagtc cccggaagag cctgcgcagc tgaagcagag tgcttctaga 691  
 tggagagtgg tcaactgggga aaaggacctg gccatcacct tccaatacct gctgcctgtc 751  
 tccctgaccc atgatctggc aagttaggca cagtcagaca tggacagttg atccatgagg 811  
 aaaagatgct ctcccaccta aggccaggaa tctgagagca ggactggctg agctcccagg 871  
 gcaagggggtt cactaatgct tatcaataaa gaatattgag cctgg 916

<210> 120  
 <211> 107  
 <212> PRT  
 <213> Homo sapiens

<400> 120  
 Met Gly Arg Lys Arg Leu Ile Thr Asp Ser Tyr Pro Val Val Lys Arg  
 1 5 10 15  
 Arg Glu Gly Pro Ala Gly His Ser Lys Gly Glu Leu Ala Pro Glu Leu  
 20 25 30  
 Gly Glu Glu Pro Gln Pro Arg Asp Glu Glu Glu Ala Glu Leu Glu Leu  
 35 40 45  
 Leu Arg Gln Phe Asp Leu Ala Trp Gln Tyr Gly Pro Cys Thr Gly Ile  
 50 55 60  
 Thr Arg Leu Gln Arg Trp Cys Arg Ala Lys Gln Met Gly Leu Glu Pro  
 65 70 75 80  
 Pro Pro Glu Val Trp Gln Val Leu Lys Thr His Pro Gly Asp Pro Arg  
 85 90 95  
 Phe Gln Cys Ser Leu Trp His Leu Tyr Pro Leu  
 100 105

<210> 121  
 <211> 1002  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (51)..(731)

<400> 121  
 ctattttctc acctggttcc cgcggcgagc cagcggcagc ggcggcggcg atg aga 56  
 Met Arg

1

cag aag cac tac ctt gag gct gca gcg cgg gga ctg cac gac agc tgc	104
Gln Lys His Tyr Leu Glu Ala Ala Arg Gly Leu His Asp Ser Cys	
5 10 15	
ccg ggc caa gcc cgc tac ctc ctt ctc ttt ctc ttt tac agc tgg gcc	152
Pro Gly Gln Ala Arg Tyr Leu Leu Leu Phe Leu Phe Tyr Ser Trp Ala	
20 25 30	
tac act tcg tcg cac gat gat aag agc act ttt gaa gaa acg tgt cca	200
Tyr Thr Ser Ser His Asp Asp Lys Ser Thr Phe Glu Glu Thr Cys Pro	
35 40 45 50	
tac tgt ttc cag ctg ttg gtt ctg gat aac tct cga gtg cgt ctc aaa	248
Tyr Cys Phe Gln Leu Leu Val Leu Asp Asn Ser Arg Val Arg Leu Lys	
55 60 65	
ccc aaa gcc agg ttg aca ccc aaa ata cag aaa ctt ctt aat cga gaa	296
Pro Lys Ala Arg Leu Thr Pro Lys Ile Gln Lys Leu Leu Asn Arg Glu	
70 75 80	
gcg aga aac tat aca ctc agt ttt aaa gaa gca aaa atg gtg aaa aag	344
Ala Arg Asn Tyr Thr Leu Ser Phe Lys Glu Ala Lys Met Val Lys Lys	
85 90 95	
ttc aaa gac tcc aaa agt gta ttg ttg atc act tgt aaa aca tgc aac	392
Phe Lys Asp Ser Lys Ser Val Leu Leu Ile Thr Cys Lys Thr Cys Asn	
100 105 110	
aga aca gtg aaa cat cat ggt aaa agt aga agc ttt gtg tca aca ttg	440
Arg Thr Val Lys His His Gly Lys Ser Arg Ser Phe Val Ser Thr Leu	
115 120 125 130	
aag agc aat cct gcc act cct aca agt aaa ctc agc ctg aag aca cca	488
Lys Ser Asn Pro Ala Thr Pro Thr Ser Lys Leu Ser Leu Lys Thr Pro	
135 140 145	
gag aga agg act gca aac cca aat cat gac atg tct ggc tcg aaa ggc	536
Glu Arg Arg Thr Ala Asn Pro Asn His Asp Met Ser Gly Ser Lys Gly	
150 155 160	
aag agc cca gca tcg gtt ttc aga aca cct aca tct gga cag tca gta	584
Lys Ser Pro Ala Ser Val Phe Arg Thr Pro Thr Ser Gly Gln Ser Val	
165 170 175	
tct act tgc tcc tca aag aac acc agc aaa aca aag aaa cac ttc tct	632
Ser Thr Cys Ser Ser Lys Asn Thr Ser Lys Thr Lys Lys His Phe Ser	
180 185 190	
caa cta aaa atg tta ctt agt cag aat gaa tcc caa aag att cca aag	680
Gln Leu Lys Met Leu Ser Gln Asn Glu Ser Gln Lys Ile Pro Lys	
195 200 205 210	
gtg gac ttc aga aat ttc tta tct tct ctg aag ggt gga ctt tta aaa	728
Val Asp Phe Arg Asn Phe Leu Ser Ser Leu Lys Gly Gly Leu Leu Lys	
215 220 225	

taa gaaatgcctg atgtcaattc tgaaactaaa gttggtaaaa caacttttta 781  
aactcttatt cattttttga atacatggaa actagatctg aatgcaaact tttcttggca 841  
tccttcagtg tttatgggga aaatacctca ttagtgtgaa tacctgaaac ctgcctacct 901  
cataggacag ctgtgaggat caaaaaatat atgaaagttc cttgtagata catatctata 961  
gatatatatg tgtatgtata taaagataga tatatacatt g 1002

<210> 122  
<211> 226  
<212> PRT  
<213> Homo sapiens

<400> 122  
Met Arg Gln Lys His Tyr Leu Glu Ala Ala Arg Gly Leu His Asp  
1 5 10 15  
Ser Cys Pro Gly Gln Ala Arg Tyr Leu Leu Phe Leu Phe Tyr Ser  
20 25 30  
Trp Ala Tyr Thr Ser Ser His Asp Asp Lys Ser Thr Phe Glu Glu Thr  
35 40 45  
Cys Pro Tyr Cys Phe Gln Leu Leu Val Leu Asp Asn Ser Arg Val Arg  
50 55 60  
Leu Lys Pro Lys Ala Arg Leu Thr Pro Lys Ile Gln Lys Leu Leu Asn  
65 70 75 80  
Arg Glu Ala Arg Asn Tyr Thr Leu Ser Phe Lys Glu Ala Lys Met Val  
85 90 95  
Lys Lys Phe Lys Asp Ser Lys Ser Val Leu Leu Ile Thr Cys Lys Thr  
100 105 110  
Cys Asn Arg Thr Val Lys His His Gly Lys Ser Arg Ser Phe Val Ser  
115 120 125  
Thr Leu Lys Ser Asn Pro Ala Thr Pro Thr Ser Lys Leu Ser Leu Lys  
130 135 140  
Thr Pro Glu Arg Arg Thr Ala Asn Pro Asn His Asp Met Ser Gly Ser  
145 150 155 160  
Lys Gly Lys Ser Pro Ala Ser Val Phe Arg Thr Pro Thr Ser Gly Gln  
165 170 175  
Ser Val Ser Thr Cys Ser Ser Lys Asn Thr Ser Lys Thr Lys Lys His  
180 185 190  
Phe Ser Gln Leu Lys Met Leu Leu Ser Gln Asn Glu Ser Gln Lys Ile  
195 200 205  
Pro Lys Val Asp Phe Arg Asn Phe Leu Ser Ser Leu Lys Gly Gly Leu  
210 215 220  
Leu Lys  
225

<210> 123  
<211> 1753  
<212> DNA  
<213> Homo sapiens

<220>

<221> CDS

<222> (268)..(1455)

<400> 123

gcctttgtttt acaaccctgc catgatctcc ctcttgcaaa agcgagggct acagaacagg 60

cattcaggag tcctgtgctc cagtcacagc cttttctgtt cttcagctag gagacaccaa 120

accctcagga agatttacta tagctaagag aaaactgcag cagaaagggc gcggtacct 180

acttcttaaa ttccgtttgt ggaccctcag actcttagtc ccctactccc agatacagcg 240

gccctaccgt ggctcctggc aagaagc atg gat ctc gga atc cct gac ctg ctg 294

Met Asp Leu Gly Ile Pro Asp Leu Leu

1

5

gac gcg tgg ctg gag ccc cca gag gat atc ttc tcg aca gga tcc gtc 342

Asp Ala Trp Leu Glu Pro Pro Glu Asp Ile Phe Ser Thr Gly Ser Val

10

15

20

25

ctg gag ctg gga ctc cac tgc ccc cct cca gag gtt ccg gta act agg 390

Leu Glu Leu Gly Leu His Cys Pro Pro Pro Glu Val Pro Val Thr Arg

30

35

40

cta cag gaa cag gga ctg caa ggc tgg aag tcc ggt ggg gac cgt ggc 438

Leu Gln Glu Gln Gly Leu Gln Gly Trp Lys Ser Gly Gly Asp Arg Gly

45

50

55

tgt ggc ctt caa gag agt gag cct gaa gat ttc ttg aag ctt ttc att 486

Cys Gly Leu Gln Glu Ser Glu Pro Glu Asp Phe Leu Lys Leu Phe Ile

60

65

70

gat ccc aat gag gtg tac tgc tca gaa gca tct cct ggc agt gac agt 534

Asp Pro Asn Glu Val Tyr Cys Ser Glu Ala Ser Pro Gly Ser Asp Ser

75

80

85

ggc atc tct gag gac ccc tgc cat cca gac agt ccc cct gcc ccc agg 582

Gly Ile Ser Glu Asp Pro Cys His Pro Asp Ser Pro Pro Ala Pro Arg

90

95

100

105

gca acc agt tct cct atg ctc tat gag gtt gtc tat gag gca ggg gcc 630

Ala Thr Ser Ser Pro Met Leu Tyr Glu Val Val Tyr Glu Ala Gly Ala

110

115

120

ctg gag agg atg cag ggg gaa act ggg cca aat gta ggc ctt atc tcc 678

Leu Glu Arg Met Gln Gly Glu Thr Gly Pro Asn Val Gly Leu Ile Ser

125

130

135

atc cag cta gat cag tgg agc cca gca ttt atg gtg cct gat tcc tgc 726

Ile Gln Leu Asp Gln Trp Ser Pro Ala Phe Met Val Pro Asp Ser Cys

140

145

150

atg gtc agt gag ctg ccc ttt gat gct cat gcc cac atc ctg ccc aga 774

Met Val Ser Glu Leu Pro Phe Asp Ala His Ala His Ile Leu Pro Arg

155

160

165

gca ggc acc gta gcc cca gtg ccc tgt aca acc ctg ctg ccc tgt caa 822

09890688.092701

Ala Gly Thr Val Ala Pro Val Pro Cys Thr Thr Leu Leu Pro Cys Gln	
170 175 180 185	
acc ctg ttc ctg acc gat gag gag aag cgt ctg ctg ggg cag gaa ggg	870
Thr Leu Phe Leu Thr Asp Glu Glu Lys Arg Leu Leu Gly Gln Glu Gly	
190 195 200	
gtt tcc ctg ccc tct cac ctg ccc ctc acc aag gca gag gag agg gtc	918
Val Ser Leu Pro Ser His Leu Pro Leu Thr Lys Ala Glu Glu Arg Val	
205 210 215	
ctc aag aag gtc agg agg aaa atc cgt aac aag cag tca gct cag gac	966
Leu Lys Lys Val Arg Arg Lys Ile Arg Asn Lys Gln Ser Ala Gln Asp	
220 225 230	
agt cgg cgg cgg aag aag gag tac att gat ggg ctg gag agc agg gtg	1014
Ser Arg Arg Arg Lys Lys Glu Tyr Ile Asp Gly Leu Glu Ser Arg Val	
235 240 245	
gca gcc tgt tct gca cag aac caa gaa tta cag aaa aaa gtc cag gag	1062
Ala Ala Cys Ser Ala Gln Asn Gln Glu Leu Gln Lys Lys Val Gln Glu	
250 255 260 265	
ctg gag agg cac aac atc tcc ttg gta gct cag ctc cgc cag ctg cag	1110
Leu Glu Arg His Asn Ile Ser Leu Val Ala Gln Leu Arg Gln Leu Gln	
270 275 280	
acg cta att gct caa act tcc aac aaa gct gcc cag acc agc act tgt	1158
Thr Leu Ile Ala Gln Thr Ser Asn Lys Ala Ala Gln Thr Ser Thr Cys	
285 290 295	
gtt ttg att ctt ctt ttt tcc ctg gct ctc atc atc ctg ccc agc ttc	1206
Val Leu Ile Leu Leu Phe Ser Leu Ala Leu Ile Ile Leu Pro Ser Phe	
300 305 310	
agt cca ttc cag agt cga cca gaa gct ggg tct gag gat tac cag cct	1254
Ser Pro Phe Gln Ser Arg Pro Glu Ala Gly Ser Glu Asp Tyr Gln Pro	
315 320 325	
cac gga gtg act tcc aga aat atc ctg acc cac aag gac gta aca gaa	1302
His Gly Val Thr Ser Arg Asn Ile Leu Thr His Lys Asp Val Thr Glu	
330 335 340 345	
aat ctg gag acc caa gtg gta gag tcc aga ctg agg gag cca cct gga	1350
Asn Leu Glu Thr Gln Val Val Glu Ser Arg Leu Arg Glu Pro Pro Gly	
350 355 360	
gcc aag gat gca aat ggc tca aca agg aca ctg ctt gag aag atg gga	1398
Ala Lys Asp Ala Asn Gly Ser Thr Arg Thr Leu Leu Glu Lys Met Gly	
365 370 375	
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Gly Lys Pro Arg Pro Ser Gly Arg Ile Arg Ser Val Leu His Ala Asp	
380 385 390	
gag atg tga gctggaacag accttctctgg cccacttctt gatcacaagg	1495
Glu Met	



395

aatcctgggc ttccttatgg ctttgcttcc cactgggatt cctacttagg tgtctgcct 1555  
 caggggtcca aatcacttca ggacacccca agagatgtcc tttagtctct gcctgaggcc 1615  
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 Pro Pro Pro Glu Val Pro Val Thr Arg Leu Gln Glu Gln Gly Leu Gln  
 35 40 45  
 Gly Trp Lys Ser Gly Gly Asp Arg Gly Cys Gly Leu Gln Glu Ser Glu  
 50 55 60  
 Pro Glu Asp Phe Leu Lys Leu Phe Ile Asp Pro Asn Glu Val Tyr Cys  
 65 70 75 80  
 Ser Glu Ala Ser Pro Gly Ser Asp Ser Gly Ile Ser Glu Asp Pro Cys  
 85 90 95  
 His Pro Asp Ser Pro Pro Ala Pro Arg Ala Thr Ser Ser Pro Met Leu  
 100 105 110  
 Tyr Glu Val Val Tyr Glu Ala Gly Ala Leu Glu Arg Met Gln Gly Glu  
 115 120 125  
 Thr Gly Pro Asn Val Gly Leu Ile Ser Ile Gln Leu Asp Gln Trp Ser  
 130 135 140  
 Pro Ala Phe Met Val Pro Asp Ser Cys Met Val Ser Glu Leu Pro Phe  
 145 150 155 160  
 Asp Ala His Ala His Ile Leu Pro Arg Ala Gly Thr Val Ala Pro Val  
 165 170 175  
 Pro Cys Thr Thr Leu Leu Pro Cys Gln Thr Leu Phe Leu Thr Asp Glu  
 180 185 190  
 Glu Lys Arg Leu Leu Gly Gln Glu Gly Val Ser Leu Pro Ser His Leu  
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 Pro Leu Thr Lys Ala Glu Glu Arg Val Leu Lys Lys Val Arg Arg Lys  
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 Ile Arg Asn Lys Gln Ser Ala Gln Asp Ser Arg Arg Arg Lys Lys Glu  
 225 230 235 240  
 Tyr Ile Asp Gly Leu Glu Ser Arg Val Ala Ala Cys Ser Ala Gln Asn  
 245 250 255  
 Gln Glu Leu Gln Lys Lys Val Gln Glu Leu Glu Arg His Asn Ile Ser  
 260 265 270  
 Leu Val Ala Gln Leu Arg Gln Leu Gln Thr Leu Ile Ala Gln Thr Ser  
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 Asn Lys Ala Ala Gln Thr Ser Thr Cys Val Leu Ile Leu Leu Phe Ser  
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0990688-092701

09890688.092701

Leu Ala Leu Ile Ile Leu Pro Ser Phe Ser Pro Phe Gln Ser Arg Pro  
 305 310 315 320  
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 325 330 335  
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 340 345 350  
 Glu Ser Arg Leu Arg Glu Pro Pro Gly Ala Lys Asp Ala Asn Gly Ser  
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 Ala Pro Gly Cys Gly Arg Val Val Ser His Ala Gly Ala Pro Gly Gly  
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gga acg cgg cca ccc tga gtctggtgag tcgactgcgg cggcctgtgt 152  
 Gly Thr Arg Pro Pro  
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09890688-092701

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Ile Leu Gln Arg Val Pro Gly Lys Gln Arg Phe Gly Ile Tyr Arg Phe  
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Leu Pro Phe Phe Phe Val Leu Gly Gly Thr Met Glu Trp Ile Met Ile  
30 35 40  
  
aaa gtg cgc gtg ggc cag gag acc ttc tat gat gtc tac cgt aga aaa 197  
Lys Val Arg Val Gly Gln Glu Thr Phe Tyr Asp Val Tyr Arg Arg Lys  
45 50 55  
  
gcc tca gaa aga cag tat cag aga agg ctg gaa gat gaa tga 239  
Ala Ser Glu Arg Gln Tyr Gln Arg Arg Leu Glu Asp Glu  
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Gly Gly Thr Met Glu Trp Ile Met Ile Lys Val Arg Val Gly Gln Glu  
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Met Glu Glu Lys Pro Gly Gln Pro  
1 5  
cag cct cag cac cat cac agc cac cac cat ccg cac cat cac cct cag 162  
Gln Pro Gln His His His Ser His His His Pro His His His Pro Gln  
10 15 20  
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Gln Gln Gln Gln Gln Pro His His His His His Tyr Tyr Phe Tyr Asn  
25 30 35 40  
cac agc cac aac cac cac cac cac cat cat cac cag cag cct cac caa 258  
His Ser His Asn His His His His His His His Gln Gln Pro His Gln  
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tac ctg cag cat gga gcc gag ggc agc ccc aag gcc cag cca aag ccg 306  
Tyr Leu Gln His Gly Ala Glu Gly Ser Pro Lys Ala Gln Pro Lys Pro  
60 65 70  
ctg aaa cat gag cag aaa cac acc ctc cag cag cac cag gaa acg ccg 354  
Leu Lys His Glu Gln Lys His Thr Leu Gln Gln His Gln Glu Thr Pro  
75 80 85  
aag aag aaa aca ggc tat ggt gaa cta aac ggt aat gct gga gaa aga 402  
Lys Lys Lys Thr Gly Tyr Gly Glu Leu Asn Gly Asn Ala Gly Glu Arg  
90 95 100  
gaa ata tct tta aag aac ctg agt tct gat gaa gcc acc aac cct att 450  
Glu Ile Ser Leu Lys Asn Leu Ser Ser Asp Glu Ala Thr Asn Pro Ile  
105 110 115 120  
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Ser Arg Val Leu Asn Gly Asn Gln Gln Val Val Asp Thr Ser Leu Lys  
125 130 135  
cag act gta aag gcc aac acc ttt ggg aaa gca gga att aaa acc aag 546  
Gln Thr Val Lys Ala Asn Thr Phe Gly Lys Ala Gly Ile Lys Thr Lys  
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09890688.092701

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Glu Asn Lys Ser Gly Glu Asn Gln Ser Val Asp Lys Ser Asp Thr Ile	
170 175 180	
cca att cca aat ggt gtg gta aca aat aat tct ggt tat att act aat	690
Pro Ile Pro Asn Gly Val Val Thr Asn Asn Ser Gly Tyr Ile Thr Asn	
185 190 195 200	
ggt tat atg agt aaa gga gca gat aat gat ggt agt gga tct gag agc	738
Gly Tyr Met Ser Lys Gly Ala Asp Asn Asp Gly Ser Gly Ser Glu Ser	
205 210 215	
gga tat aca act cct aaa aaa agg aaa gct agg cgc aat agt gcc aag	786
Gly Tyr Thr Thr Pro Lys Lys Arg Lys Ala Arg Arg Asn Ser Ala Lys	
220 225 230	
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Gly Cys Glu Asn Leu Asn Ile Val Gln Asp Lys Ile Met Gln Gln Glu	
235 240 245	
acc agt gtc cca acc tta aaa cag gga ctt gaa act ttc aag cct gac	882
Thr Ser Val Pro Thr Leu Lys Gln Gly Leu Glu Thr Phe Lys Pro Asp	
250 255 260	
tat agt gaa caa aag gga aat cga gta gat ggt tcg aag ccc att tgg	930
Tyr Ser Glu Gln Lys Gly Asn Arg Val Asp Gly Ser Lys Pro Ile Trp	
265 270 275 280	
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Lys Tyr Glu Thr Gly Pro Gly Gly Thr Ser Arg Gly Lys Pro Ala Val	
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Gly Asp Met Leu Arg Lys Ser Ser Asp Ser Lys Pro Gly Val Ser Ser	
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Lys Lys Phe Asp Asp Arg Pro Lys Gly Lys His Ala Ser Ala Val Ala	
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Ser Lys Glu Asp Ser Trp Thr Leu Phe Lys Pro Pro Pro Val Phe Pro	
330 335 340	
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Val Asp Asn Ser Ser Ala Lys Ile Val Pro Lys Ile Ser Tyr Ala Ser	
345 350 355 360	
aaa gtt aag gaa aac ctc aac aaa act ata cag aac tct tct gtg tca	1218
Lys Val Lys Glu Asn Leu Asn Lys Thr Ile Gln Asn Ser Ser Val Ser	
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Pro Thr Ser Ser Ser Ser Ser Ser Ser Ser Thr Gly Glu Thr Gln Thr	

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caa tca tca agt cgc tta tcc	cag gtc cct atg tca gcg ctg aaa tct		1314
Gln Ser Ser Ser Arg Leu Ser	Gln Val Pro Met Ser Ala Leu Lys Ser		
395	400	405	
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Val Thr Ser Ala Asn Phe Ser	Asn Gly Pro Val Leu Ala Gly Thr Asp		
410	415	420	
gga aat gtt tat cct cca ggg ggt	cag cca ctg cta act act gct gct		1410
Gly Asn Val Tyr Pro Pro Gly	Gly Gln Pro Leu Leu Thr Thr Ala Ala		
425	430	435	440
aat act cta aca ccc atc tct tct	ggg aca gat tca gtt ctc cag gac		1458
Asn Thr Leu Thr Pro Ile Ser Ser	Gly Thr Asp Ser Val Leu Gln Asp		
445	450	455	
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Met Ser Leu Thr Ser Ala Ala Val	Glu Gln Ile Lys Thr Ser Leu Phe		
460	465	470	
atc tat cct tca aat atg caa act	atg ctg ttg agc aca gca caa gtg		1554
Ile Tyr Pro Ser Asn Met Gln Thr	Met Leu Leu Ser Thr Ala Gln Val		
475	480	485	
gat ctg ccc tct cag aca gat	cag caa aac ctg ggg gat atc ttc cag		1602
Asp Leu Pro Ser Gln Thr Asp Gln	Gln Asn Leu Gly Asp Ile Phe Gln		
490	495	500	
aat cag tgg ggt tta tca ttt ata	aat gag ccc agt gct ggc cct gag		1650
Asn Gln Trp Gly Leu Ser Phe Ile	Asn Glu Pro Ser Ala Gly Pro Glu		
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act gtt act ggg aag tca tca gag	cat aaa gtg atg gag gtg aca ttt		1698
Thr Val Thr Gly Lys Ser Ser Glu	His Lys Val Met Glu Val Thr Phe		
525	530	535	
caa gga gaa tat cct gct act ttg	gtt tca cag ggt gct gaa ata att		1746
Gln Gly Glu Tyr Pro Ala Thr Leu	Val Ser Gln Gly Ala Glu Ile Ile		
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ccc tca gga act gag cat cct gtg	ttt ccc aag gct tac gag ctg gag		1794
Pro Ser Gly Thr Glu His Pro Val	Phe Pro Lys Ala Tyr Glu Leu Glu		
555	560	565	
aaa cgg act agt cct caa gtt ctg	ggt agc att cta aaa tct ggg act		1842
Lys Arg Thr Ser Pro Gln Val Leu	Gly Ser Ile Leu Lys Ser Gly Thr		
570	575	580	
act agt gag agt gga gcc tta tcc	ttg gaa ccc agt cat ata ggt gac		1890
Thr Ser Glu Ser Gly Ala Leu Ser	Leu Glu Pro Ser His Ile Gly Asp		
585	590	595	600
ctg cag aaa gca gac acc agt agt	caa ggt gct tta gtg ttt ctc tca		1938
Leu Gln Lys Ala Asp Thr Ser Ser	Gln Gly Ala Leu Val Phe Leu Ser		
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act ttg tta ggc tct gcc aaa gaa cag aga tac cag aga ggc cta gaa 2034  
 Thr Leu Leu Gly Ser Ala Lys Glu Gln Arg Tyr Gln Arg Gly Leu Glu  
 635 640 645

agg aat gat agc tgg ggt tct ttt gac ctg agg gct gct att gta tat 2082  
 Arg Asn Asp Ser Trp Gly Ser Phe Asp Leu Arg Ala Ala Ile Val Tyr  
 650 655 660

cac act aaa gaa atg gaa tct att tgg aat ttg cag aag caa gat ccc 2130  
 His Thr Lys Glu Met Glu Ser Ile Trp Asn Leu Gln Lys Gln Asp Pro  
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 Lys Arg Ile Ile Thr Tyr Asn Glu Ala Met Asp Ser Pro Asp Gln  
 685 690 695

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<212> PRT

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<400> 130

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			20					25					30		
His	His	His	Tyr	Tyr	Phe	Tyr	Asn	His	Ser	His	Asn	His	His	His	His
			35				40					45			
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	65				70					75					80
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	145				150				155						160
Asp	Lys	Lys	Asn	Gly	Lys	Ser	Tyr	Glu	Asn	Lys	Ser	Gly	Glu	Asn	Gln
			165					170						175	
Ser	Val	Asp	Lys	Ser	Asp	Thr	Ile	Pro	Ile	Pro	Asn	Gly	Val	Val	Thr
		180					185						190		
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		195					200					205			
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	210					215					220				
Lys	Ala	Arg	Arg	Asn	Ser	Ala	Lys	Gly	Cys	Glu	Asn	Leu	Asn	Ile	Val
	225				230					235					240
Gln	Asp	Lys	Ile	Met	Gln	Gln	Glu	Thr	Ser	Val	Pro	Thr	Leu	Lys	Gln
			245						250					255	
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		260						265					270		
Val	Asp	Gly	Ser	Lys	Pro	Ile	Trp	Lys	Tyr	Glu	Thr	Gly	Pro	Gly	Gly
	275						280					285			
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	290					295					300				
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	305				310					315					320
Gly	Lys	His	Ala	Ser	Ala	Val	Ala	Ser	Lys	Glu	Asp	Ser	Trp	Thr	Leu
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Phe	Lys	Pro	Pro	Pro	Val	Phe	Pro	Val	Asp	Asn	Ser	Ser	Ala	Lys	Ile
		340						345					350		
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09890688.092701



09890688.092701

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Gly Pro Val Leu Ala Gly Thr Asp Gly Asn Val Tyr Pro Pro Gly Gly
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Gln Pro Leu Leu Thr Thr Ala Ala Asn Thr Leu Thr Pro Ile Ser Ser
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Gly Thr Asp Ser Val Leu Gln Asp Met Ser Leu Thr Ser Ala Ala Val
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Glu Gln Ile Lys Thr Ser Leu Phe Ile Tyr Pro Ser Asn Met Gln Thr
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Gln Asn Leu Gly Asp Ile Phe Gln Asn Gln Trp Gly Leu Ser Phe Ile
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His Lys Val Met Glu Val Thr Phe Gln Gly Glu Tyr Pro Ala Thr Leu
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Val Ser Gln Gly Ala Glu Ile Ile Pro Ser Gly Thr Glu His Pro Val
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Phe Pro Lys Ala Tyr Glu Leu Glu Lys Arg Thr Ser Pro Gln Val Leu
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Gly Ser Ile Leu Lys Ser Gly Thr Thr Ser Glu Ser Gly Ala Leu Ser
                               580                               585                               590
Leu Glu Pro Ser His Ile Gly Asp Leu Gln Lys Ala Asp Thr Ser Ser
595                               600                               605
Gln Gly Ala Leu Val Phe Leu Ser Lys Asp Tyr Glu Ile Glu Ser Gln
610                               615                               620
Asn Pro Leu Ala Ser Pro Thr Asn Thr Leu Leu Gly Ser Ala Lys Glu
625                               630                               635                               640
Gln Arg Tyr Gln Arg Gly Leu Glu Arg Asn Asp Ser Trp Gly Ser Phe
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Asp Leu Arg Ala Ala Ile Val Tyr His Thr Lys Glu Met Glu Ser Ile
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09890688-092701

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Lys His Leu Phe Asn Leu Lys Phe Ala Ala Lys Glu Leu Ser Arg Ser						
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gcc aaa aaa tgc gat aag gag gaa aag gcc gaa aag gcc aaa att aaa						210
Ala Lys Lys Cys Asp Lys Glu Glu Lys Ala Glu Lys Ala Lys Ile Lys						
	25			30	35	
aag gcc att cag aag ggc aac atg gaa gtt gcg agg ata cac gcc gaa						258
Lys Ala Ile Gln Lys Gly Asn Met Glu Val Ala Arg Ile His Ala Glu						
	40			45	50	
aat gcc atc cgc cag aag aac cag gcg gtg aat ttc ttg aga atg agt						306
Asn Ala Ile Arg Gln Lys Asn Gln Ala Val Asn Phe Leu Arg Met Ser						
	55			60	65	
gcg cga gtc gat gca gtg gct gcc agg gtc cag acg gcg gtg acg atg						354
Ala Arg Val Asp Ala Val Ala Ala Arg Val Gln Thr Ala Val Thr Met						
	70			75	80	85
ggc aag gtg acc aag tgc atg gct ggt gtg gtt aag tgc atg gat gcg						402
Gly Lys Val Thr Lys Ser Met Ala Gly Val Val Lys Ser Met Asp Ala						
	90			95	100	
aca ttg aag acc atg aat ctg gag aag att tct gct ttg atg gac aaa						450
Thr Leu Lys Thr Met Asn Leu Glu Lys Ile Ser Ala Leu Met Asp Lys						
	105			110	115	
ttc gag cac cag ttt gag act ctg gac gtc cag acg cag caa atg gaa						498
Phe Glu His Gln Phe Glu Thr Leu Asp Val Gln Thr Gln Gln Met Glu						
	120			125	130	
gac acg atg agc agc acg acg acg ctc acc act ccc cag aac caa gtg						546
Asp Thr Met Ser Ser Thr Thr Thr Leu Thr Thr Pro Gln Asn Gln Val						
	135			140	145	
gat atg ctg ctc cag gaa atg gca gat gag gcg ggc ctc gac ctc aac						594
Asp Met Leu Leu Gln Glu Met Ala Asp Glu Ala Gly Leu Asp Leu Asn						
	150			155	160	165
atg gag ctg ccg cag ggc cag acc ggc tcc gtg ggc acg agc gtg gct						642
Met Glu Leu Pro Gln Gly Gln Thr Gly Ser Val Gly Thr Ser Val Ala						
	170			175	180	
tcg gcg gag cag gat gaa ctg tct cag aga ctg gcc cgc ctt cgg gat						690
Ser Ala Glu Gln Asp Glu Leu Ser Gln Arg Leu Ala Arg Leu Arg Asp						
	185			190	195	
caa gtg tga cggcagaacc cgctctgagg tttcctggcc atagccaccc						739
Gln Val						
tttgaaatgc tctctgtgtg ttagagagat actataccct agaaactctg aacacgccag						799
aatgctgaaa tgcccttcta cctttgggtt tacagccccc tccacataaa ttaagaaatt						859

cagtatttct gcactcttag ctggattcta aagttctgta tagctcgtaa tgatgggtatt 919  
 tttatagcag ccttttaaca gaactagtta atttcgtgta tatgaatctt tctcgaagat 979  
 ctgggtcaaaa ctgtattcag tttcctgccc agaatgatca gattgaaggt gggtgggtttt 1039  
 tattattatt tagtgtgatt gatagtatct agaatggcag gtgggtgcata aaagttaaag 1099  
 agaggggaaa gattacttag tttggttata cagttataaa caccatgcag tgtattcggt 1159  
 ggactgtgct atttctgttt atcctttggg ttttgggtttt tgtttttttt ttttgccttc 1219  
 acagtgcagac tgcaaatgat tgttctcata acgtatatta ttaataaatg tggtcctata 1279  
 atttatactg g 1290

<210> 132  
 <211> 199  
 <212> PRT  
 <213> Homo sapiens

<400> 132  
 Met Ser Asn Met Glu Lys His Leu Phe Asn Leu Lys Phe Ala Ala Lys  
 1 5 10 15  
 Glu Leu Ser Arg Ser Ala Lys Lys Cys Asp Lys Glu Glu Lys Ala Glu  
 20 25 30  
 Lys Ala Lys Ile Lys Lys Ala Ile Gln Lys Gly Asn Met Glu Val Ala  
 35 40 45  
 Arg Ile His Ala Glu Asn Ala Ile Arg Gln Lys Asn Gln Ala Val Asn  
 50 55 60  
 Phe Leu Arg Met Ser Ala Arg Val Asp Ala Val Ala Ala Arg Val Gln  
 65 70 75 80  
 Thr Ala Val Thr Met Gly Lys Val Thr Lys Ser Met Ala Gly Val Val  
 85 90 95  
 Lys Ser Met Asp Ala Thr Leu Lys Thr Met Asn Leu Glu Lys Ile Ser  
 100 105 110  
 Ala Leu Met Asp Lys Phe Glu His Gln Phe Glu Thr Leu Asp Val Gln  
 115 120 125  
 Thr Gln Gln Met Glu Asp Thr Met Ser Ser Thr Thr Thr Leu Thr Thr  
 130 135 140  
 Pro Gln Asn Gln Val Asp Met Leu Leu Gln Glu Met Ala Asp Glu Ala  
 145 150 155 160  
 Gly Leu Asp Leu Asn Met Glu Leu Pro Gln Gly Gln Thr Gly Ser Val  
 165 170 175  
 Gly Thr Ser Val Ala Ser Ala Glu Gln Asp Glu Leu Ser Gln Arg Leu  
 180 185 190  
 Ala Arg Leu Arg Asp Gln Val  
 195

<210> 133  
 <211> 564  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (24)..(380)

<400> 133

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gcctgccggg agcttggtgc gct atg gcg aca ccc agc ctg cgg ggt cgt ctg 53
      Met Ala Thr Pro Ser Leu Arg Gly Arg Leu
            1             5             10

gcg cgg ttt ggg aac ccg cgg aag cct gtg ctg aag ccc aat aaa cct 101
Ala Arg Phe Gly Asn Pro Arg Lys Pro Val Leu Lys Pro Asn Lys Pro
            15             20             25

ctc att cta gct aac cgc gtc ggg gag cgg cgc cgg gag aag ggc gag 149
Leu Ile Leu Ala Asn Arg Val Gly Glu Arg Arg Arg Glu Lys Gly Glu
            30             35             40

gcg act tgc atc acg gag atg tcg gtg atg atg gct tgc tgg aag cag 197
Ala Thr Cys Ile Thr Glu Met Ser Val Met Met Ala Cys Trp Lys Gln
            45             50             55

aat gaa ttc cgc gac gat gcg tgc aga aaa gag atc cag ggc ttc ctc 245
Asn Glu Phe Arg Asp Asp Ala Cys Arg Lys Glu Ile Gln Gly Phe Leu
            60             65             70

gat tgt gcc gcg agg gct cag gaa gcc cga aag atg aga tca ata cag 293
Asp Cys Ala Ala Arg Ala Gln Glu Ala Arg Lys Met Arg Ser Ile Gln
            75             80             85             90

gaa acc ctg gga gag tct ggg agt tta ctt cca aat aaa ttg aat aag 341
Glu Thr Leu Gly Glu Ser Gly Ser Leu Leu Pro Asn Lys Leu Asn Lys
            95             100             105

ttg tta cag agg ttt cct aac aaa cct tac ctc agc tga aaatggacaa 390
Leu Leu Gln Arg Phe Pro Asn Lys Pro Tyr Leu Ser
            110             115

gtattttcaa tgactgaaat atagcttctg acaactatgc agaggcattt tagagacatt 450

ggcattgccca tgccctcttt ggagggtaga agaggcaaaa cacttttttc acccttttga 510

atcatagtat gggtagaagt tatgatttat cttgaaataa aatcctctga acag 564
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<210> 134  
 <211> 118  
 <212> PRT  
 <213> Homo sapiens

<400> 134

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Met Ala Thr Pro Ser Leu Arg Gly Arg Leu Ala Arg Phe Gly Asn Pro
      1             5             10             15
Arg Lys Pro Val Leu Lys Pro Asn Lys Pro Leu Ile Leu Ala Asn Arg
            20             25             30
Val Gly Glu Arg Arg Arg Glu Lys Gly Glu Ala Thr Cys Ile Thr Glu
            35             40             45
Met Ser Val Met Met Ala Cys Trp Lys Gln Asn Glu Phe Arg Asp Asp
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      50              55              60
Ala Cys Arg Lys Glu Ile Gln Gly Phe Leu Asp Cys Ala Ala Arg Ala
 65              70              75              80
Gln Glu Ala Arg Lys Met Arg Ser Ile Gln Glu Thr Leu Gly Glu Ser
      85              90              95
Gly Ser Leu Leu Pro Asn Lys Leu Asn Lys Leu Leu Gln Arg Phe Pro
      100              105              110
Asn Lys Pro Tyr Leu Ser
      115

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<210> 135  
 <211> 904  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (467)..(811)

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<400> 135
actctgcgtg cgccggaggc tgccgtggcg ggtgggccgc ctgacttctc ctcccggcca 60

gtttctcgagc gcctcaccgg gcctcgccct gcagcctcgc tctcgctggc gctgcgcggc 120

ctaggggact gggctgctgg cctccgggtg cgggggtggg gcaggctccg acctggggcg 180

tcctggccgc gcgagccgcg ggatgggggc cggggccgcg gaggaggcgc cgctggtgtg 240

tcccttggtg gagagggcgc tgccggccct gcgcggtttc cagccaggaa gcttcgggaa 300

gcctggacgt ctgctcactg gagatgacac gtgcgtgggg tgttggcatt cttgttattt 360

aacacgggaa ggaggtgact tcgcctgtga tggacttcca gtgtgagcac tggccagagt 420

gaccaggctg accagcacca gccctgatcc agatgcagag gccagg atg tgg gcc 475
                               Met Trp Ala
                               1

cag ccc tgt gcc agg agg ctg gct gga ata aag gta cag ata gag gcc 523
Gln Pro Cys Ala Arg Arg Leu Ala Gly Ile Lys Val Gln Ile Glu Ala
 5              10              15

tca ccc cct ctg gga cca ctg gca ctc agg gtg ttt gca gcc tca gag 571
Ser Pro Pro Leu Gly Pro Leu Ala Leu Arg Val Phe Ala Ala Ser Glu
 20              25              30              35

ccc acc tgc ccc cag ggc cac agc tgc atc tcc tgc cct gct gtc att 619
Pro Thr Cys Pro Gln Gly His Ser Cys Ile Ser Cys Pro Ala Val Ile
      40              45              50

aca ggg atg ggc agg ctg gca tgg ggg cac ccg ctg ccc ctg cct ggg 667
Thr Gly Met Gly Arg Leu Ala Trp Gly His Pro Leu Pro Leu Pro Gly
      55              60              65

tgt tgc tgt gta ttc ctg ccg gcc agg ggc cac tgc cag gac cac gcc 715
Cys Cys Cys Val Phe Leu Pro Ala Arg Gly His Cys Gln Asp His Ala

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09890688.092701

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              70              75              80
tcc ctt ttc ata tcc cga ttc tta agt tct gct att gtg gta ttc tgg 763
Ser Leu Phe Ile Ser Arg Phe Leu Ser Ser Ala Ile Val Val Phe Trp
      85              90              95

tgg aga aaa aag aac cgc gtg gct gtt ttt gaa ctg cct gga acc taa 811
Trp Arg Lys Lys Asn Arg Val Ala Val Phe Glu Leu Pro Gly Thr
100              105              110

gaccctgaat tcttttcccc cccaagggga aaatctatat ggaaaacatt tattttaaaa 871

tacaggatga agtgaattaa aagatttaaa tgc 904

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<210> 136  
 <211> 114  
 <212> PRT  
 <213> Homo sapiens

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<400> 136
Met Trp Ala Gln Pro Cys Ala Arg Arg Leu Ala Gly Ile Lys Val Gln
  1              5              10              15
Ile Glu Ala Ser Pro Pro Leu Gly Pro Leu Ala Leu Arg Val Phe Ala
      20              25              30
Ala Ser Glu Pro Thr Cys Pro Gln Gly His Ser Cys Ile Ser Cys Pro
      35              40              45
Ala Val Ile Thr Gly Met Gly Arg Leu Ala Trp Gly His Pro Leu Pro
      50              55              60
Leu Pro Gly Cys Cys Cys Val Phe Leu Pro Ala Arg Gly His Cys Gln
      65              70              75              80
Asp His Ala Ser Leu Phe Ile Ser Arg Phe Leu Ser Ser Ala Ile Val
      85              90              95
Val Phe Trp Trp Arg Lys Lys Asn Arg Val Ala Val Phe Glu Leu Pro
      100              105              110
Gly Thr

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<210> 137  
 <211> 472  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (90)..(353)

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<400> 137
aatttcgct tccggtagtg agaacccttc cggtgggcta ggtactgagc gcgcgaggct 60

ctacagagtg aaggtttaaa tccaaggctc atg gca aaa cat ctg aag ttc atc 113
              Met Ala Lys His Leu Lys Phe Ile
              1              5

gcc agg act gtg atg gta cag gaa ggg aac gtg gaa agc gca tac agg 161
Ala Arg Thr Val Met Val Gln Glu Gly Asn Val Glu Ser Ala Tyr Arg

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10              15              20
acc cta aac aga atc ctc act atg gat ggg ctc att gag gac att aag 209
Thr Leu Asn Arg Ile Leu Thr Met Asp Gly Leu Ile Glu Asp Ile Lys
25              30              35              40

cat cgg cgg tat tat gag aag cca tgc cgc cgg cga cag agg gaa agc 257
His Arg Arg Tyr Tyr Glu Lys Pro Cys Arg Arg Arg Gln Arg Glu Ser
45              50              55

tat gaa agg tgc cgg cgg atc tac aac atg gaa atg gct cgc aag atc 305
Tyr Glu Arg Cys Arg Arg Ile Tyr Asn Met Glu Met Ala Arg Lys Ile
60              65              70

aac ttc ttg atg cga aag aat cgg gca gat ccg tgg cag ggc tgc tga 353
Asn Phe Leu Met Arg Lys Asn Arg Ala Asp Pro Trp Gln Gly Cys
75              80              85

ggcctgtggg tgggacaccc agtgcgaaac cctcatccag ttttctctcc atctcttttc 413
tttgtacaat cccatttcct attaccattc tctgcaataa actcaaatca catgtctgc 472

<210> 138
<211> 87
<212> PRT
<213> Homo sapiens

<400> 138
Met Ala Lys His Leu Lys Phe Ile Ala Arg Thr Val Met Val Gln Glu
1              5              10              15
Gly Asn Val Glu Ser Ala Tyr Arg Thr Leu Asn Arg Ile Leu Thr Met
20              25              30
Asp Gly Leu Ile Glu Asp Ile Lys His Arg Arg Tyr Tyr Glu Lys Pro
35              40              45
Cys Arg Arg Arg Gln Arg Glu Ser Tyr Glu Arg Cys Arg Arg Ile Tyr
50              55              60
Asn Met Glu Met Ala Arg Lys Ile Asn Phe Leu Met Arg Lys Asn Arg
65              70              75              80
Ala Asp Pro Trp Gln Gly Cys
85

<210> 139
<211> 180
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (49)..(168)

<400> 139
attatatatg aattccattc aaatcgttcc tttttgttaa caaggggc atg ggg agg 57
Met Gly Arg
1

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09890688.092701

ggt ggg ggt ggg ggg gca gag gcg tct gac ccc agg aac ctg cag ggc 105  
 Gly Gly Gly Gly Gly Ala Glu Ala Ser Asp Pro Arg Asn Leu Gln Gly  
           5                  10                  15

ggg gct ggg tcg gtg ccc tct aag gac aat ttt gac ctt gtt caa cct 153  
 Gly Ala Gly Ser Val Pro Ser Lys Asp Asn Phe Asp Leu Val Gln Pro  
           20                  25                  30                  35

ttc cac aaa gaa taa attgtgtttc ac 180  
 Phe His Lys Glu

<210> 140  
 <211> 39  
 <212> PRT  
 <213> Homo sapiens

<400> 140  
 Met Gly Arg Gly Gly Gly Gly Ala Glu Ala Ser Asp Pro Arg Asn  
   1                  5                  10                  15  
 Leu Gln Gly Gly Ala Gly Ser Val Pro Ser Lys Asp Asn Phe Asp Leu  
           20                  25                  30  
 Val Gln Pro Phe His Lys Glu  
           35

<210> 141  
 <211> 473  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (35)..(343)

<400> 141  
 gagacgcaga gtcttgagca gcgcggcagg cacc atg ttc ctg act gcg ctc ctc 55  
   Met Phe Leu Thr Ala Leu Leu  
   1                  5

tgg cgc ggc cgc att ccc ggc cgt cag tgg atc ggg aag cac cgg cgg 103  
 Trp Arg Gly Arg Ile Pro Gly Arg Gln Trp Ile Gly Lys His Arg Arg  
           10                  15                  20

ccg cgg ttc gtg tcg ttg cgc gcc aag cag aac atg atc cgc cgc ctg 151  
 Pro Arg Phe Val Ser Leu Arg Ala Lys Gln Asn Met Ile Arg Arg Leu  
           25                  30                  35

gag atc gag gcg gag aac cat tac tgg ctg agc atg ccc tac atg acc 199  
 Glu Ile Glu Ala Glu Asn His Tyr Trp Leu Ser Met Pro Tyr Met Thr  
           40                  45                  50                  55

cgg gag cag gag cgc ggc cac gcc gcg gtg cgc agg agg gag gcc ttc 247  
 Arg Glu Gln Glu Arg Gly His Ala Ala Val Arg Arg Arg Glu Ala Phe  
           60                  65                  70





agc	gtc	atc	cag	aac	ctg	ccc	aag	aac	ggt	tct	tac	cgc	ccc	tcc	tat	213
Ser	Val	Ile	Gln	Asn	Leu	Pro	Lys	Asn	Gly	Ser	Tyr	Arg	Pro	Ser	Tyr	
			25						30			35				
gaa	gag	atg	ctg	cga	ttc	tac	agt	tac	tac	aag	cag	gcc	acc	atg	ggg	261
Glu	Glu	Met	Leu	Arg	Phe	Tyr	Ser	Tyr	Tyr	Lys	Gln	Ala	Thr	Met	Gly	
			40						45			50				
ccc	tgc	ctg	gtc	ccc	cgg	ccc	ggg	ttc	tgg	gac	ccc	att	gga	cga	tat	309
Pro	Cys	Leu	Val	Pro	Arg	Pro	Gly	Phe	Trp	Asp	Pro	Ile	Gly	Arg	Tyr	
			55						60			65				
aag	tgg	gac	gcc	tgg	aac	agt	ctg	ggc	aag	atg	agc	agg	gag	gag	gcc	357
Lys	Trp	Asp	Ala	Trp	Asn	Ser	Leu	Gly	Lys	Met	Ser	Arg	Glu	Glu	Ala	
			70			75						80				
atg	tct	gcc	tac	atc	act	gaa	atg	aaa	ctg	gtg	gca	cag	aag	gtg	atc	405
Met	Ser	Ala	Tyr	Ile	Thr	Glu	Met	Lys	Leu	Val	Ala	Gln	Lys	Val	Ile	
			85			90						95			100	
gac	aca	gtg	ccc	ctg	ggt	gag	gtg	gca	gag	gac	atg	ttt	ggt	tac	ttc	453
Asp	Thr	Val	Pro	Leu	Gly	Glu	Val	Ala	Glu	Asp	Met	Phe	Gly	Tyr	Phe	
			105						110			115				
gag	ccc	ctg	tac	cag	gtg	atc	cct	gac	atg	ccg	agg	ccc	cca	gag	acc	501
Glu	Pro	Leu	Tyr	Gln	Val	Ile	Pro	Asp	Met	Pro	Arg	Pro	Pro	Glu	Thr	
			120						125			130				
ttc	ctg	aga	agg	gtc	aca	ggt	tgg	aaa	gag	cag	gtt	gtg	aat	gga	gat	549
Phe	Leu	Arg	Arg	Val	Thr	Gly	Trp	Lys	Glu	Gln	Val	Val	Asn	Gly	Asp	
			135			140						145				
gtt	ggg	gct	gtt	tca	gag	cct	ccc	tgc	ctc	ccc	aag	gaa	ccg	gca	ccc	597
Val	Gly	Ala	Val	Ser	Glu	Pro	Pro	Cys	Leu	Pro	Lys	Glu	Pro	Ala	Pro	
			150			155						160				
cca	agc	cca	gct	tcc	ctc	tgg	gca	gta	act	cta	cca	acc	cct	cca	cag	645
Pro	Ser	Pro	Ala	Ser	Leu	Trp	Ala	Val	Thr	Leu	Pro	Thr	Pro	Pro	Gln	
			165			170			175			180				
agt	ccc	att	cac	cca	ggg	acc	tgg	act	ccg	agg	ttt	tct	gtg	att	ccc	693
Ser	Pro	Ile	His	Pro	Gly	Thr	Trp	Thr	Pro	Arg	Phe	Ser	Val	Ile	Pro	
			185						190			195				
tgg	agc	agc	tgg	agc	ctg	agc	tgg	ttt	gga	cag	agc	agc	ggg	cag	cat	741
Trp	Ser	Ser	Trp	Ser	Leu	Ser	Trp	Phe	Gly	Gln	Ser	Ser	Gly	Gln	His	
			200						205			210				
ctg	gag	gaa	agc	gtg	atc	cca	gga	aca	gcc	ccg	tgc	ccc	cca	caa	aga	789
Leu	Glu	Glu	Ser	Val	Ile	Pro	Gly	Thr	Ala	Pro	Cys	Pro	Pro	Gln	Arg	
			215			220						225				
aag	agg	ggt	tgc	ggg	gca	gcc	cgc	cgg	ggc	ccc	agg	agt	tgg	acg	tgt	837
Lys	Arg	Gly	Cys	Gly	Ala	Ala	Arg	Arg	Gly	Pro	Arg	Ser	Trp	Thr	Cys	
			230			235						240				
ggc	tgc	tgg	gga	cag	ttc	gaq	cac	tac	agg	aga	gca	tgc	agg	agg	tgc	885

Gly Cys Trp Gly Gln Phe Glu His Tyr Arg Arg Ala Cys Arg Arg Cys  
 245 250 255 260

agg cga ggg tgc aga gcc tgg aga gca tgc ccc ggc ccc ctg agc aga 933  
 Arg Arg Gly Cys Arg Ala Trp Arg Ala Cys Pro Gly Pro Leu Ser Arg  
 265 270 275

ggc cgc agc cca ggc cca gtg ctc ggc cat ggc ccc ttg ggc tcc cgg 981  
 Gly Arg Ser Pro Gly Pro Val Leu Gly His Gly Pro Leu Gly Ser Arg  
 280 285 290

ggc ccg cgc tgc tct tct tcc tcc tgt ggc cct tcg tcg tcc agt ggc 1029  
 Gly Pro Arg Cys Ser Ser Ser Ser Cys Gly Pro Ser Ser Ser Ser Gly  
 295 300 305

tct tcc gaa tgt ttc gga ccc aaa aga ggt gac tgt cag tgg agg ggt 1077  
 Ser Ser Glu Cys Phe Gly Pro Lys Arg Gly Asp Cys Gln Trp Arg Gly  
 310 315 320

ctc tgc agc caa ctg aga cta tct tgc tgt gcc ctg agc ctt cct agg 1125  
 Leu Cys Ser Gln Leu Arg Leu Ser Cys Cys Ala Leu Ser Leu Pro Arg  
 325 330 335 340

gtt tag aagaacagca ttcaaaattc cccgtcctgt cagtgtttgc ctctgcacct 1181  
 Val

cctcccctaa agcagcgcg ggggcaaata agaccccacc cctccctgca gcttcacagg 1241

gacgcttcct tccctccccg caaccacccc aggcctccct gggaggctgc agttgtggta 1301

cacgtccccg gtgctggggt ggccgtgact cgggggcggg gcgatcggt ctcagcccct 1361

gccttcccga gtctctgggt caccgaatt ttccacccc tgettctccc cgaggagggt 1421

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gcgggaggga ggccaggagg cccggaccag ttgggaggag tgagcaggcc ccgggggagg 1541

gggatgagcg cagtttgctc gctttcctcc cctgccggcc cctccgccc ccacacacac 1601

tcgggacgtc ttcattgaag attcacttac aaaggaatgt ttactaaat aaaagaaaac 1661

cag 1664

<210> 144  
 <211> 341  
 <212> PRT  
 <213> Homo sapiens

<400> 144  
 Met Gly Thr Glu Lys Glu Ser Pro Glu Pro Asp Cys Gln Lys Gln Phe  
 1 5 10 15  
 Gln Ala Ala Val Ser Val Ile Gln Asn Leu Pro Lys Asn Gly Ser Tyr  
 20 25 30  
 Arg Pro Ser Tyr Glu Glu Met Leu Arg Phe Tyr Ser Tyr Tyr Lys Gln  
 35 40 45

10260" 0990688 092701

Ala Thr Met Gly Pro Cys Leu Val Pro Arg Pro Gly Phe Trp Asp Pro  
 50 55 60  
 Ile Gly Arg Tyr Lys Trp Asp Ala Trp Asn Ser Leu Gly Lys Met Ser  
 65 70 75 80  
 Arg Glu Glu Ala Met Ser Ala Tyr Ile Thr Glu Met Lys Leu Val Ala  
 85 90 95  
 Gln Lys Val Ile Asp Thr Val Pro Leu Gly Glu Val Ala Glu Asp Met  
 100 105 110  
 Phe Gly Tyr Phe Glu Pro Leu Tyr Gln Val Ile Pro Asp Met Pro Arg  
 115 120 125  
 Pro Pro Glu Thr Phe Leu Arg Arg Val Thr Gly Trp Lys Glu Gln Val  
 130 135 140  
 Val Asn Gly Asp Val Gly Ala Val Ser Glu Pro Pro Cys Leu Pro Lys  
 145 150 155 160  
 Glu Pro Ala Pro Pro Ser Pro Ala Ser Leu Trp Ala Val Thr Leu Pro  
 165 170 175  
 Thr Pro Pro Gln Ser Pro Ile His Pro Gly Thr Trp Thr Pro Arg Phe  
 180 185 190  
 Ser Val Ile Pro Trp Ser Ser Trp Ser Leu Ser Trp Phe Gly Gln Ser  
 195 200 205  
 Ser Gly Gln His Leu Glu Glu Ser Val Ile Pro Gly Thr Ala Pro Cys  
 210 215 220  
 Pro Pro Gln Arg Lys Arg Gly Cys Gly Ala Ala Arg Arg Gly Pro Arg  
 225 230 235 240  
 Ser Trp Thr Cys Gly Cys Trp Gly Gln Phe Glu His Tyr Arg Arg Ala  
 245 250 255  
 Cys Arg Arg Cys Arg Arg Gly Cys Arg Ala Trp Arg Ala Cys Pro Gly  
 260 265 270  
 Pro Leu Ser Arg Gly Arg Ser Pro Gly Pro Val Leu Gly His Gly Pro  
 275 280 285  
 Leu Gly Ser Arg Gly Pro Arg Cys Ser Ser Ser Ser Cys Gly Pro Ser  
 290 295 300  
 Ser Ser Ser Gly Ser Ser Glu Cys Phe Gly Pro Lys Arg Gly Asp Cys  
 305 310 315 320  
 Gln Trp Arg Gly Leu Cys Ser Gln Leu Arg Leu Ser Cys Cys Ala Leu  
 325 330 335  
 Ser Leu Pro Arg Val  
 340

<210> 145

<211> 835

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (90)..(740)

<400> 145

aaaaatccga agtgccgcgg aaagtggaga gctgacaagg aaggtttcga gcgttttgct 60

ggcaaggga tttcttataa cctccaggc atg cgt ctt tct gcc ctg ctg gcc 113  
 Met Arg Leu Ser Ala Leu Leu Ala  
 1 5

ttg gca tcc aag gtc act ctg ccc ccc cat tac cgc tat ggg atg agc 161

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Leu	Ala	Ser	Lys	Val	Thr	Leu	Pro	Pro	His	Tyr	Arg	Tyr	Gly	Met	Ser		
10						15					20						
ccc	cca	ggc	tct	gtt	gca	gac	aag	agg	aag	aac	ccc	cca	tgg	atc	agg	209	
Pro	Pro	Gly	Ser	Val	Ala	Asp	Lys	Arg	Lys	Asn	Pro	Pro	Trp	Ile	Arg		
25					30					35					40		
cgg	cgc	cca	gtg	gtt	gtg	gaa	ccc	atc	tct	gat	gaa	gac	tgg	tat	ctg	257	
Arg	Arg	Pro	Val	Val	Val	Glu	Pro	Ile	Ser	Asp	Glu	Asp	Trp	Tyr	Leu		
				45				50						55			
ttc	tgt	ggg	gac	acg	gtg	gag	atc	cta	gaa	ggc	aag	gat	gcc	ggg	aag	305	
Phe	Cys	Gly	Asp	Thr	Val	Glu	Ile	Leu	Glu	Gly	Lys	Asp	Ala	Gly	Lys		
			60					65					70				
cag	ggc	aaa	gtg	gtt	caa	gtt	atc	cgg	cag	cga	aac	tgg	gtg	gtc	gtg	353	
Gln	Gly	Lys	Val	Val	Gln	Val	Ile	Arg	Gln	Arg	Asn	Trp	Val	Val	Val		
		75					80					85					
gga	ggg	ctg	aac	aca	cat	tac	cgc	tac	att	ggc	aag	acc	atg	gat	tac	401	
Gly	Gly	Leu	Asn	Thr	His	Tyr	Arg	Tyr	Ile	Gly	Lys	Thr	Met	Asp	Tyr		
		90				95					100						
cgg	gga	acc	atg	atc	cct	agt	gaa	gcc	ccc	ttg	ctc	cac	cgc	cag	gtc	449	
Arg	Gly	Thr	Met	Ile	Pro	Ser	Glu	Ala	Pro	Leu	Leu	His	Arg	Gln	Val		
105					110					115					120		
aaa	ctt	gtg	gat	cct	atg	gac	agg	aaa	ccc	act	gag	atc	gag	tgg	aga	497	
Lys	Leu	Val	Asp	Pro	Met	Asp	Arg	Lys	Pro	Thr	Glu	Ile	Glu	Trp	Arg		
				125					130					135			
ttt	act	gaa	gca	gga	gag	cgg	gta	cga	gtc	tcc	aca	cga	tca	ggg	aga	545	
Phe	Thr	Glu	Ala	Gly	Glu	Arg	Val	Arg	Val	Ser	Thr	Arg	Ser	Gly	Arg		
			140					145					150				
att	atc	cct	aaa	ccc	gaa	ttt	ccc	aga	gct	gat	ggc	atc	gtc	cct	gaa	593	
Ile	Ile	Pro	Lys	Pro	Glu	Phe	Pro	Arg	Ala	Asp	Gly	Ile	Val	Pro	Glu		
		155					160					165					
acg	tgg	att	gat	ggc	ccc	aaa	gac	aca	tca	gtg	gaa	gat	gct	tta	gaa	641	
Thr	Trp	Ile	Asp	Gly	Pro	Lys	Asp	Thr	Ser	Val	Glu	Asp	Ala	Leu	Glu		
		170				175					180						
aga	acc	tat	gtg	ccc	tgt	cta	aag	aca	ctg	cag	gag	gag	gtg	atg	gag	689	
Arg	Thr	Tyr	Val	Pro	Cys	Leu	Lys	Thr	Leu	Gln	Glu	Glu	Val	Met	Glu		
185					190					195					200		
gcc	atg	ggg	atc	aag	gag	acc	cgg	aaa	tac	aag	aag	gtc	tat	tgg	tat	737	
Ala	Met	Gly	Ile	Lys	Glu	Thr	Arg	Lys	Tyr	Lys	Lys	Val	Tyr	Trp	Tyr		
				205					210					215			
tga	gcctggggca	gagcagctcc	tccccaactt	ctgtcccagc	cttgaaggct											790	
gaggcacttc	tttttcagat	gccaataaag	agcactttat	gagtc												835	

09890688-092701

<210> 146  
 <211> 216  
 <212> PRT  
 <213> Homo sapiens

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 Arg Lys Asn Pro Pro Trp Ile Arg Arg Pro Val Val Val Glu Pro  
 35 40 45  
 Ile Ser Asp Glu Asp Trp Tyr Leu Phe Cys Gly Asp Thr Val Glu Ile  
 50 55 60  
 Leu Glu Gly Lys Asp Ala Gly Lys Gln Gly Lys Val Val Gln Val Ile  
 65 70 75 80  
 Arg Gln Arg Asn Trp Val Val Val Gly Gly Leu Asn Thr His Tyr Arg  
 85 90 95  
 Tyr Ile Gly Lys Thr Met Asp Tyr Arg Gly Thr Met Ile Pro Ser Glu  
 100 105 110  
 Ala Pro Leu Leu His Arg Gln Val Lys Leu Val Asp Pro Met Asp Arg  
 115 120 125  
 Lys Pro Thr Glu Ile Glu Trp Arg Phe Thr Glu Ala Gly Glu Arg Val  
 130 135 140  
 Arg Val Ser Thr Arg Ser Gly Arg Ile Ile Pro Lys Pro Glu Phe Pro  
 145 150 155 160  
 Arg Ala Asp Gly Ile Val Pro Glu Thr Trp Ile Asp Gly Pro Lys Asp  
 165 170 175  
 Thr Ser Val Glu Asp Ala Leu Glu Arg Thr Tyr Val Pro Cys Leu Lys  
 180 185 190  
 Thr Leu Gln Glu Glu Val Met Glu Ala Met Gly Ile Lys Glu Thr Arg  
 195 200 205  
 Lys Tyr Lys Lys Val Tyr Trp Tyr  
 210 215

<210> 147  
 <211> 2465  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (71)..(1261)

<400> 147  
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 Met Lys Ala Val Lys Ser Glu Arg Glu Arg Gly Ser Arg  
 1 5 10  
 cga aga cac cgg gac ggg gac gtg gtg ctg ccg gcg ggg gtg gtg gtg 157  
 Arg Arg His Arg Asp Gly Asp Val Val Leu Pro Ala Gly Val Val Val  
 15 20 25  
 aag cag gag cgt ctc agc cca gaa gtc gca cct ccc gcc cac cgc cgt 205

Lys	Gln	Glu	Arg	Leu	Ser	Pro	Glu	Val	Ala	Pro	Pro	Ala	His	Arg	Arg		
30					35					40					45		
ccg	gac	cac	tcc	ggt	ggt	agc	ccg	tct	ccg	ccg	acc	agc	gag	ccg	gcc	253	
Pro	Asp	His	Ser	Gly	Gly	Ser	Pro	Ser	Pro	Pro	Thr	Ser	Glu	Pro	Ala		
				50					55					60			
cgc	tcg	ggc	cac	cgc	ggg	aac	cga	gcc	cga	gga	gtt	agc	cgg	tcc	cca	301	
Arg	Ser	Gly	His	Arg	Gly	Asn	Arg	Ala	Arg	Gly	Val	Ser	Arg	Ser	Pro		
			65					70					75				
ccc	aaa	aag	aaa	aac	aag	gcc	tca	ggg	aga	aga	agc	aag	tct	cct	cgc	349	
Pro	Lys	Lys	Lys	Asn	Lys	Ala	Ser	Gly	Arg	Arg	Ser	Lys	Ser	Pro	Arg		
		80					85					90					
agt	aag	aga	aac	cga	agt	cct	cac	cac	tca	aca	gtc	aaa	gtg	aag	cag	397	
Ser	Lys	Arg	Asn	Arg	Ser	Pro	His	His	Ser	Thr	Val	Lys	Val	Lys	Gln		
	95					100					105						
gag	cgt	gag	gat	cat	ccc	cgg	aga	gga	cgg	gag	gat	cgg	cag	cac	agg	445	
Glu	Arg	Glu	Asp	His	Pro	Arg	Arg	Gly	Arg	Glu	Asp	Arg	Gln	His	Arg		
110					115					120					125		
gaa	cca	tca	gaa	cag	gaa	cac	agg	aga	gct	agg	aac	agt	gac	cgg	gac	493	
Glu	Pro	Ser	Glu	Gln	Glu	His	Arg	Arg	Ala	Arg	Asn	Ser	Asp	Arg	Asp		
				130					135					140			
aga	cac	cgg	ggc	cat	tcc	cac	caa	agg	aga	acg	tct	aac	gag	agg	cct	541	
Arg	His	Arg	Gly	His	Ser	His	Gln	Arg	Arg	Thr	Ser	Asn	Glu	Arg	Pro		
			145					150					155				
ggg	agt	ggg	cag	ggt	cag	gga	cgg	gat	cga	gac	act	cag	aac	ctg	cag	589	
Gly	Ser	Gly	Gln	Gly	Gln	Gly	Arg	Asp	Arg	Asp	Thr	Gln	Asn	Leu	Gln		
		160					165					170					
gct	cag	gaa	gaa	gag	cgg	gag	ttt	tat	aat	gcc	agg	cga	cgg	gag	cat	637	
Ala	Gln	Glu	Glu	Glu	Arg	Glu	Phe	Tyr	Asn	Ala	Arg	Arg	Arg	Glu	His		
	175					180					185						
cgc	cag	agg	aat	gac	gtt	ggt	ggt	ggc	ggc	agt	gag	tct	cag	gag	ttg	685	
Arg	Gln	Arg	Asn	Asp	Val	Gly	Gly	Gly	Gly	Ser	Glu	Ser	Gln	Glu	Leu		
190					195					200					205		
gtt	cct	cgg	cct	ggt	ggc	aac	aac	aaa	gaa	aaa	gag	gtg	ccc	gct	aaa	733	
Val	Pro	Arg	Pro	Gly	Gly	Asn	Asn	Lys	Glu	Lys	Glu	Val	Pro	Ala	Lys		
				210					215					220			
gaa	aaa	cca	agc	ttt	gaa	ctt	tct	ggg	gca	ctt	ctt	gag	gac	acc	aac	781	
Glu	Lys	Pro	Ser	Phe	Glu	Leu	Ser	Gly	Ala	Leu	Leu	Glu	Asp	Thr	Asn		
			225					230					235				
act	ttc	cgg	ggt	gta	gtc	att	aaa	tat	agt	gag	ccc	cca	gaa	gca	cgt	829	
Thr	Phe	Arg	Gly	Val	Val	Ile	Lys	Tyr	Ser	Glu	Pro	Pro	Glu	Ala	Arg		
		240					245					250					
atc	ccc	aaa	aaa	cgg	tgg	cgt	ctc	tac	cca	ttt	aaa	aat	gat	gag	gtg	877	
Ile	Pro	Lys	Lys	Arg	Trp	Arg	Leu	Tyr	Pro	Phe	Lys	Asn	Asp	Glu	Val		

09890688.092701

255	260	265	
ctt cca gtc atg tac	ata cat cga cag agt gcg	tac cta ctg ggt cga	925
Leu Pro Val Met Tyr	Ile His Arg Gln Ser	Ala Tyr Leu Leu Gly Arg	
270	275	280 285	
cac cgc cgc att gca gac att cca att gat	cac ccg tct tgt tca aag		973
His Arg Arg Ile Ala Asp Ile Pro Ile Asp	His Pro Ser Cys Ser Lys		
	290 295	300	
cag cat gcg gtc ttt caa tat cgg ctt gtg gaa tat acc cgt gct gat			1021
Gln His Ala Val Phe Gln Tyr Arg Leu Val Glu Tyr Thr Arg Ala Asp			
	305 310	315	
ggc aca gtt ggc cga aga gtg aag ccc tac atc att gac ctt ggc tca			1069
Gly Thr Val Gly Arg Arg Val Lys Pro Tyr Ile Ile Asp Leu Gly Ser			
	320 325	330	
ggc aat gga acc ttc tta aac aac aaa cgt att gag cca cag aga tac			1117
Gly Asn Gly Thr Phe Leu Asn Asn Lys Arg Ile Glu Pro Gln Arg Tyr			
	335 340	345	
tat gaa cta aaa gaa aag gat gta ctc aaa ttt gga ttc agt agc aga			1165
Tyr Glu Leu Lys Glu Lys Asp Val Leu Lys Phe Gly Phe Ser Ser Arg			
	350 355	360 365	
gaa tac gtc ttg ctc cat gag tcg tcg gac act tct gaa ata gac agg			1213
Glu Tyr Val Leu Leu His Glu Ser Ser Asp Thr Ser Glu Ile Asp Arg			
	370 375	380	
aaa gat gac gag gat gag gag gag gag gaa gaa gtg tct gac agc tag			1261
Lys Asp Asp Glu Asp Glu Glu Glu Glu Glu Glu Val Ser Asp Ser			
	385 390	395	
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ttaagtcttt cctctgttgc tgaccagatt gtgttaccat ttgaatacac tgactaatgt			1441
ttgttaaact ttttctgtgg caccttggcc acatgcctgc aggcatttgt tttcagaaca			1501
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tcagaactgc tgcctaggaa actataaacc cttggttaag gggaaatcat ggcttgttct			1621
ctttgtacag ttactttatt tatataggtg ttaagctttg tggaccaggt gtttttcttt			1681
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agtatatacc aaagctttga cttgtttgag ctcttgagct tagaagttga ttttgactt			1801
atttttttgg ggggtgggaa tgtactgcag tcagtaaaca ttattgactg ttttaactta			1861
acagatgctt tatggcacct gctcaagccc gtgactgtac agaaggatcc tgggtgctac			1921
cagtgggtgc tgattcagca tcacaagtga ctgaaattgg ctgtggatct gttctttgtg			1981



aaagaattcc tgatttctcc atggagcatg tacacaacaa ttttgatcat attaactgta 2041  
cttcagtttt gcatttttat tcaaattgta tctctttttt tctttgagaa ataaactgtc 2101  
actgatgtga cagcgttctt tctttattct aataacatgt atagatctaa agcaggttgt 2161  
gttgtttaca tgtttctaca catttcatcc tttaaaaagt tgttgagaga ggttgtattt 2221  
accttcccaa ggttggaaag caggggaatt tccagtgtc ctagttttcc accagaggaa 2281  
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atat 2465

<210> 148  
<211> 396  
<212> PRT  
<213> Homo sapiens

<400> 148  
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Arg Leu Ser Pro Glu Val Ala Pro Pro Ala His Arg Arg Pro Asp His  
35 40 45  
Ser Gly Gly Ser Pro Ser Pro Thr Ser Glu Pro Ala Arg Ser Gly  
50 55 60  
His Arg Gly Asn Arg Ala Arg Gly Val Ser Arg Ser Pro Pro Lys Lys  
65 70 75 80  
Lys Asn Lys Ala Ser Gly Arg Arg Ser Lys Ser Pro Arg Ser Lys Arg  
85 90 95  
Asn Arg Ser Pro His His Ser Thr Val Lys Val Lys Gln Glu Arg Glu  
100 105 110  
Asp His Pro Arg Arg Gly Arg Glu Asp Arg Gln His Arg Glu Pro Ser  
115 120 125  
Glu Gln Glu His Arg Arg Ala Arg Asn Ser Asp Arg Asp Arg His Arg  
130 135 140  
Gly His Ser His Gln Arg Arg Thr Ser Asn Glu Arg Pro Gly Ser Gly  
145 150 155 160  
Gln Gly Gln Gly Arg Asp Arg Asp Thr Gln Asn Leu Gln Ala Gln Glu  
165 170 175  
Glu Glu Arg Glu Phe Tyr Asn Ala Arg Arg Arg Glu His Arg Gln Arg  
180 185 190  
Asn Asp Val Gly Gly Gly Gly Ser Glu Ser Gln Glu Leu Val Pro Arg  
195 200 205  
Pro Gly Gly Asn Asn Lys Glu Lys Glu Val Pro Ala Lys Glu Lys Pro  
210 215 220  
Ser Phe Glu Leu Ser Gly Ala Leu Leu Glu Asp Thr Asn Thr Phe Arg  
225 230 235 240  
Gly Val Val Ile Lys Tyr Ser Glu Pro Pro Glu Ala Arg Ile Pro Lys

09890688.092701

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                245                250                255
Lys Arg Trp Arg Leu Tyr Pro Phe Lys Asn Asp Glu Val Leu Pro Val
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Met Tyr Ile His Arg Gln Ser Ala Tyr Leu Leu Gly Arg His Arg Arg
                275                280                285
Ile Ala Asp Ile Pro Ile Asp His Pro Ser Cys Ser Lys Gln His Ala
                290                295                300
Val Phe Gln Tyr Arg Leu Val Glu Tyr Thr Arg Ala Asp Gly Thr Val
305                310                315                320
Gly Arg Arg Val Lys Pro Tyr Ile Ile Asp Leu Gly Ser Gly Asn Gly
                325                330                335
Thr Phe Leu Asn Asn Lys Arg Ile Glu Pro Gln Arg Tyr Tyr Glu Leu
                340                345                350
Lys Glu Lys Asp Val Leu Lys Phe Gly Phe Ser Ser Arg Glu Tyr Val
                355                360                365
Leu Leu His Glu Ser Ser Asp Thr Ser Glu Ile Asp Arg Lys Asp Asp
370                375                380
Glu Asp Glu Glu Glu Glu Glu Glu Val Ser Asp Ser
385                390                395

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<210> 149  
 <211> 3600  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (149)..(1504)

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ccctggcagg cgatgcagggt gggatgct atg gaa tat gat gag aag ctg gcc 172
                        Met Glu Tyr Asp Glu Lys Leu Ala
                        1                        5

cgt ttc cgg cag gcc cac ctc aac ccc ttc aac aag cag tct ggg ccg 220
Arg Phe Arg Gln Ala His Leu Asn Pro Phe Asn Lys Gln Ser Gly Pro
10                        15                        20

aga cag cat gag cag ggc cct ggg gag gag gtc ccg gac gtc act cct 268
Arg Gln His Glu Gln Gly Pro Gly Glu Glu Val Pro Asp Val Thr Pro
25                        30                        35                        40

gaa gag gcc ctg cct gag ctg ccc cct ggg gag ccg gaa ttc cgc tgc 316
Glu Glu Ala Leu Pro Glu Leu Pro Pro Gly Glu Glu Phe Arg Cys
45                        50                        55

cct gaa cgc gtg atg gat ctc ggc ctg tct gag gac cac ttc tcc cgc 364
Pro Glu Arg Val Met Asp Leu Gly Leu Ser Glu Asp His Phe Ser Arg
60                        65                        70

cct gtg ggt ctg ttc ctg gcc tct gac gtc cag cag ctg cgg cag gcg 412
Pro Val Gly Leu Phe Leu Ala Ser Asp Val Gln Gln Leu Arg Gln Ala

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75	80	85	
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cag gag ctg aag gac ccc aat gag gat gag cca aac atc cga gtg ctc Gln Glu Leu Lys Asp Pro Asn Glu Asp Glu Pro Asn Ile Arg Val Leu 125 130 135			556
ctt gag cac cgc ttt tac aag gag aag agc aag agc gtc aag cag acc Leu Glu His Arg Phe Tyr Lys Glu Lys Ser Lys Ser Val Lys Gln Thr 140 145 150			604
tgt gac aag tgt aac acc atc atc tgg ggg ctc att cag acc tgg tac Cys Asp Lys Cys Asn Thr Ile Ile Trp Gly Leu Ile Gln Thr Trp Tyr 155 160 165			652
acc tgc aca ggg tgt tat tac cgc tgt cac agt aag tgc ttg aac ctc Thr Cys Thr Gly Cys Tyr Tyr Arg Cys His Ser Lys Cys Leu Asn Leu 170 175 180			700
atc tcc aag ccc tgt gtg agc tcc aaa gtc agc cac caa gct gaa tac Ile Ser Lys Pro Cys Val Ser Ser Lys Val Ser His Gln Ala Glu Tyr 185 190 195 200			748
gaa ctg aac atc tgc cct gag aca ggg ctg gac agc cag gat tac cgc Glu Leu Asn Ile Cys Pro Glu Thr Gly Leu Asp Ser Gln Asp Tyr Arg 205 210 215			796
tgt gcc gag tgc cgg gcg ccc atc tct ctg cgg ggt gtg ccc agt gag Cys Ala Glu Cys Arg Ala Pro Ile Ser Leu Arg Gly Val Pro Ser Glu 220 225 230			844
gcc agg cag tgc gac tac acc ggc cag tac tac tgc agc cac tgc cac Ala Arg Gln Cys Asp Tyr Thr Gly Gln Tyr Tyr Cys Ser His Cys His 235 240 245			892
tgg aac gac ctg gct gtg atc cct gca cgc gtt gta cac aac tgg gac Trp Asn Asp Leu Ala Val Ile Pro Ala Arg Val Val His Asn Trp Asp 250 255 260			940
ttt gag cct cga aag gtt tct cgc tgc agc atg cgc tac ctg gcg ctg Phe Glu Pro Arg Lys Val Ser Arg Cys Ser Met Arg Tyr Leu Ala Leu 265 270 275 280			988
atg gtg tct cgg ccc gta ctc agg ctc cgg gag atc aac cct ctg ctg Met Val Ser Arg Pro Val Leu Arg Leu Arg Glu Ile Asn Pro Leu Leu 285 290 295			1036
ttc agc tac gtg gag gag ctg gtg gag att cgc aag ctg cgc cag gac Phe Ser Tyr Val Glu Glu Leu Val Glu Ile Arg Lys Leu Arg Gln Asp 300 305 310			1084

atc ctg ctg atg aag ccg tac ttc atc acc tgc agg gag gcc atg gag 1132  
 Ile Leu Leu Met Lys Pro Tyr Phe Ile Thr Cys Arg Glu Ala Met Glu  
 315 320 325

gct cgt ctg ctg ctg cag ctg cag gat cgg cag cat ttt gtg gag aac 1180  
 Ala Arg Leu Leu Leu Gln Leu Gln Asp Arg Gln His Phe Val Glu Asn  
 330 335 340

gac gag atg tac tct gtc cag gac ctg ctg gac gtg cat gcc ggc cgc 1228  
 Asp Glu Met Tyr Ser Val Gln Asp Leu Leu Asp Val His Ala Gly Arg  
 345 350 355 360

ctg ggc tgc tgc ctg acc gag atc cac acg ctg ttc gcc aag cac atc 1276  
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 365 370 375

aag ctg gac tgc gag cgg tgc cag gcc aag ggc ttc gtg tgt gag ctg 1324  
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tgc aga gag ggc gac gtg ctg ttc ccg ttc gac agc cac acg tct gtg 1372  
 Cys Arg Glu Gly Asp Val Leu Phe Pro Phe Asp Ser His Thr Ser Val  
 395 400 405

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 Cys Ala Asp Cys Ser Ala Val Phe His Arg Asp Cys Tyr Tyr Asp Asn  
 410 415 420

tcc acc act tgt ccc aag tgt gcc cgg ctg agc ctg agg aag cag tgc 1468  
 Ser Thr Thr Cys Pro Lys Cys Ala Arg Leu Ser Leu Arg Lys Gln Ser  
 425 430 435 440

ctc ttc cag gag cca ggt ccc gat gtg gag gcc tag cgccgaggaa 1514  
 Leu Phe Gln Glu Pro Gly Pro Asp Val Glu Ala  
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09890688-092701

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aggaaacca agaggagaca cctcagtcag cagaaaggcc acctgggtca ctgggtcatt 2894  
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gtcctgtttc cccttctct ttggggctga ggaggaggt aaaggccaaa tgctgtttcc 3194  
caacacccca aagtctgcac acgtctcatg aatgcatcac atttctgtca tatggatatt 3254  
agccattccg aaatctgtgt aatcaacttc acattattca agttacaaat cactgtgtcc 3314  
atagaaaaac tgtgtggta tttgctggac aaagggttg gccctttta tttttacctg 3374  
ccaccagca tctccccac ctgcccctt tgggtgacac agccggtaaa cggaatcacg 3434  
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tggaagacca cacatgggtg gtcccacagc atgggaccag gctggcctga gggatgcca 3554  
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09890688-092701

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Pro	Phe	Asn	Lys	Gln	Ser	Gly	Pro	Arg	Gln	His	Glu	Gln	Gly	Pro	Gly
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Glu	Glu	Val	Pro	Asp	Val	Thr	Pro	Glu	Glu	Ala	Leu	Pro	Glu	Leu	Pro
		35					40					45			
Pro	Gly	Glu	Pro	Glu	Phe	Arg	Cys	Pro	Glu	Arg	Val	Met	Asp	Leu	Gly
	50					55					60				
Leu	Ser	Glu	Asp	His	Phe	Ser	Arg	Pro	Val	Gly	Leu	Phe	Leu	Ala	Ser
	65				70					75					80
Asp	Val	Gln	Gln	Leu	Arg	Gln	Ala	Ile	Glu	Glu	Cys	Lys	Gln	Val	Ile
				85					90					95	
Leu	Glu	Leu	Pro	Glu	Gln	Ser	Glu	Lys	Gln	Lys	Asp	Ala	Val	Val	Arg
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Leu	Ile	His	Leu	Arg	Leu	Lys	Leu	Gln	Glu	Leu	Lys	Asp	Pro	Asn	Glu
		115				120						125			
Asp	Glu	Pro	Asn	Ile	Arg	Val	Leu	Leu	Glu	His	Arg	Phe	Tyr	Lys	Glu
	130					135					140				
Lys	Ser	Lys	Ser	Val	Lys	Gln	Thr	Cys	Asp	Lys	Cys	Asn	Thr	Ile	Ile
	145				150					155					160
Trp	Gly	Leu	Ile	Gln	Thr	Trp	Tyr	Thr	Cys	Thr	Gly	Cys	Tyr	Tyr	Arg
			165					170						175	
Cys	His	Ser	Lys	Cys	Leu	Asn	Leu	Ile	Ser	Lys	Pro	Cys	Val	Ser	Ser
			180					185					190		
Lys	Val	Ser	His	Gln	Ala	Glu	Tyr	Glu	Leu	Asn	Ile	Cys	Pro	Glu	Thr
		195					200					205			
Gly	Leu	Asp	Ser	Gln	Asp	Tyr	Arg	Cys	Ala	Glu	Cys	Arg	Ala	Pro	Ile
	210					215					220				
Ser	Leu	Arg	Gly	Val	Pro	Ser	Glu	Ala	Arg	Gln	Cys	Asp	Tyr	Thr	Gly
	225				230					235					240
Gln	Tyr	Tyr	Cys	Ser	His	Cys	His	Trp	Asn	Asp	Leu	Ala	Val	Ile	Pro
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Ala	Arg	Val	Val	His	Asn	Trp	Asp	Phe	Glu	Pro	Arg	Lys	Val	Ser	Arg
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Cys	Ser	Met	Arg	Tyr	Leu	Ala	Leu	Met	Val	Ser	Arg	Pro	Val	Leu	Arg
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Leu	Arg	Glu	Ile	Asn	Pro	Leu	Leu	Phe	Ser	Tyr	Val	Glu	Glu	Leu	Val
	290					295					300				
Glu	Ile	Arg	Lys	Leu	Arg	Gln	Asp	Ile	Leu	Leu	Met	Lys	Pro	Tyr	Phe
	305				310					315					320
Ile	Thr	Cys	Arg	Glu	Ala	Met	Glu	Ala	Arg	Leu	Leu	Leu	Gln	Leu	Gln
				325					330					335	
Asp	Arg	Gln	His	Phe	Val	Glu	Asn	Asp	Glu	Met	Tyr	Ser	Val	Gln	Asp
			340					345					350		
Leu	Leu	Asp	Val	His	Ala	Gly	Arg	Leu	Gly	Cys	Ser	Leu	Thr	Glu	Ile
		355					360					365			
His	Thr	Leu	Phe	Ala	Lys	His	Ile	Lys	Leu	Asp	Cys	Glu	Arg	Cys	Gln
	370					375					380				
Ala	Lys	Gly	Phe	Val	Cys	Glu	Leu	Cys	Arg	Glu	Gly	Asp	Val	Leu	Phe
				390						395					400
Pro	Phe	Asp	Ser	His	Thr	Ser	Val	Cys	Ala	Asp	Cys	Ser	Ala	Val	Phe
				405					410					415	
His	Arg	Asp	Cys	Tyr	Tyr	Asp	Asn	Ser	Thr	Thr	Cys	Pro	Lys	Cys	Ala
			420					425					430		
Arg	Leu	Ser	Leu	Arg	Lys	Gln	Ser	Leu	Phe	Gln	Glu	Pro	Gly	Pro	Asp
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Val	Glu	Ala													

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ttg tcc gga gct gcg gcc tta ggc ttc gct tcc tac ggg gcg cac ggc 98  
Leu Ser Gly Ala Ala Ala Leu Gly Phe Ala Ser Tyr Gly Ala His Gly  
15 20 25  
  
gcc caa ttc cca gat gcc tac ggg aag gag ctg ttt gac aag gcc aac 146  
Ala Gln Phe Pro Asp Ala Tyr Gly Lys Glu Leu Phe Asp Lys Ala Asn  
30 35 40 45  
  
aaa cac cac ttc tta cac agc ctg gcc ctg tta ggg gtg ccc cat tgc 194  
Lys His His Phe Leu His Ser Leu Ala Leu Leu Gly Val Pro His Cys  
50 55 60  
  
aga aag cca ctc tgg gct ggg tta ttg cta gct tcc gga acg acc tta 242  
Arg Lys Pro Leu Trp Ala Gly Leu Leu Leu Ala Ser Gly Thr Thr Leu  
65 70 75  
  
ttc tgc acc agc ttt tac tac cag gct ctg agt gga gac ccc agc atc 290  
Phe Cys Thr Ser Phe Tyr Tyr Gln Ala Leu Ser Gly Asp Pro Ser Ile  
80 85 90  
  
cag act ttg gcc cct gcg gga ggg acc ctg cta ctc ttg ggc tgg ctt 338  
Gln Thr Leu Ala Pro Ala Gly Gly Thr Leu Leu Leu Gly Trp Leu  
95 100 105  
  
gcc ttg gct ctt tga gctccctttt gcttaattac tgggttttct gggcagtttt 393  
Ala Leu Ala Leu  
110  
  
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<213> Homo sapiens

<400> 152  
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Ala Ala Ala Leu Gly Phe Ala Ser Tyr Gly Ala His Gly Ala Gln Phe





Ala	Lys	Met	Pro	Gln	Met	Ile	Val	Asn	Trp	Gln	Gln	Gln	Gln	Arg	Glu		
				130					135					140			
aac	tgg	gag	aag	gcc	cag	gct	gac	aag	gag	agg	agg	gcc	cga	ctg	cag	482	
Asn	Trp	Glu	Lys	Ala	Gln	Ala	Asp	Lys	Glu	Arg	Arg	Ala	Arg	Leu	Gln		
			145					150				155					
gct	gag	gcc	cag	gag	ctc	ctg	ggc	tac	cag	gtg	gac	cca	agg	agt	gcc	530	
Ala	Glu	Ala	Gln	Glu	Leu	Leu	Gly	Tyr	Gln	Val	Asp	Pro	Arg	Ser	Ala		
		160					165					170					
cgc	ttc	cag	gag	ctg	ctc	cag	gac	cta	gag	aag	aag	gag	cgc	aag	cgc	578	
Arg	Phe	Gln	Glu	Leu	Leu	Gln	Asp	Leu	Glu	Lys	Lys	Glu	Arg	Lys	Arg		
	175					180					185						
ctc	aag	gag	gaa	aaa	cag	aaa	cgg	aag	aag	gag	gcg	cga	gct	gct	gca	626	
Leu	Lys	Glu	Glu	Lys	Gln	Lys	Arg	Lys	Lys	Glu	Ala	Arg	Ala	Ala	Ala		
	190				195					200					205		
ttg	gct	gca	gct	gtg	gct	caa	gac	cca	gca	gcc	tct	ggg	gca	ccc	agc	674	
Leu	Ala	Ala	Ala	Val	Ala	Gln	Asp	Pro	Ala	Ala	Ser	Gly	Ala	Pro	Ser		
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Ser																	
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Thr	Leu	Ala	Pro	Gly	Ser	Arg	Gly	Tyr	Arg	Ala	Arg	Pro	Pro	Pro	Arg		
			20					25					30				
Arg	Arg	Pro	Gly	Pro	Arg	Trp	Pro	Asp	Pro	Glu	Asp	Leu	Leu	Thr	Pro		
		35					40					45					
Arg	Trp	Gln	Leu	Gly	Pro	Arg	Tyr	Ala	Ala	Lys	Gln	Phe	Ala	Arg	Tyr		
	50					55					60						
Gly	Ala	Ala	Ser	Gly	Val	Val	Pro	Gly	Ser	Leu	Trp	Pro	Ser	Pro	Glu		
	65				70					75					80		
Gln	Leu	Arg	Glu	Leu	Glu	Ala	Glu	Glu	Arg	Glu	Trp	Tyr	Pro	Ser	Leu		
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Ala	Thr	Met	Gln	Glu	Ser	Leu	Arg	Val	Lys	Gln	Leu	Ala	Glu	Glu	Gln		
			100					105					110				
Lys	Arg	Arg	Glu	Arg	Glu	Gln	His	Ile	Ala	Glu	Cys	Met	Ala	Lys	Met		
		115					120					125					
Pro	Gln	Met	Ile	Val	Asn	Trp	Gln	Gln	Gln	Gln	Arg	Glu	Asn	Trp	Glu		
	130					135					140						
Lys	Ala	Gln	Ala	Asp	Lys	Glu	Arg	Arg	Ala	Arg	Leu	Gln	Ala	Glu	Ala		
	145				150					155					160		
Gln	Glu	Leu	Leu	Gly	Tyr	Gln	Val	Asp	Pro	Arg	Ser	Ala	Arg	Phe	Gln		
				165					170					175			
Glu	Leu	Leu	Gln	Asp	Leu	Glu	Lys	Lys	Glu	Arg	Lys	Arg	Leu	Lys	Glu		
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Glu Lys Gln Lys Arg Lys Lys Glu Ala Arg Ala Ala Ala Leu Ala Ala  
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 gccgaggcct gggttacaag cagcaagtgc gcggttgggg ccaactgcgag gccgttttag 180  
 aaaactgttt aaaacaaaga gcaattg atg gat aaa tca gga ata gat tct ctt 234  
 Met Asp Lys Ser Gly Ile Asp Ser Leu  
 1 5  
 gac cat gtg aca tct gat gct gtg gaa ctt gca aat cga agt gat aac 282  
 Asp His Val Thr Ser Asp Ala Val Glu Leu Ala Asn Arg Ser Asp Asn  
 10 15 20 25  
 tct tct gat agc agc tta ttt aaa act cag tgt atc cct tac tca cct 330  
 Ser Ser Asp Ser Ser Leu Phe Lys Thr Gln Cys Ile Pro Tyr Ser Pro  
 30 35 40  
 aaa ggg gag aaa aga aac ccc att cga aaa ttt gtt cgt aca cct gaa 378  
 Lys Gly Glu Lys Arg Asn Pro Ile Arg Lys Phe Val Arg Thr Pro Glu  
 45 50 55  
 agt gtt cac gca agt gat tca tca agt gac tca tct ttt gaa cca ata 426  
 Ser Val His Ala Ser Asp Ser Ser Ser Asp Ser Ser Phe Glu Pro Ile  
 60 65 70  
 cca ttg act ata aaa gct att ttt gaa aga ttc aag aac agg aaa aag 474  
 Pro Leu Thr Ile Lys Ala Ile Phe Glu Arg Phe Lys Asn Arg Lys Lys  
 75 80 85  
 aga tat aaa aaa aag aaa aag agg agg tac cag cca aca gga aga cca 522  
 Arg Tyr Lys Lys Lys Lys Lys Arg Arg Tyr Gln Pro Thr Gly Arg Pro  
 90 95 100 105  
 cgg gga aga cca gaa gga agg aga aat cct ata tac tca cta ata gat 570  
 Arg Gly Arg Pro Glu Gly Arg Arg Asn Pro Ile Tyr Ser Leu Ile Asp  
 110 115 120  
 aag aag aaa caa ttt aga agc aga gga tct ggc ttc cca ttt tta gaa 618  
 Lys Lys Lys Gln Phe Arg Ser Arg Gly Ser Gly Phe Pro Phe Leu Glu  
 125 130 135

tca gag aat gaa aaa aac gca cct tgg aga aaa att tta acg ttt gag 666  
 Ser Glu Asn Glu Lys Asn Ala Pro Trp Arg Lys Ile Leu Thr Phe Glu  
 140 145 150

caa gct gtt gca aga gga ttt ttt aac tat att gaa aaa ctg aag tat 714  
 Gln Ala Val Ala Arg Gly Phe Phe Asn Tyr Ile Glu Lys Leu Lys Tyr  
 155 160 165

gaa cac cac ctg aaa gaa tca ttg aag caa atg aat gtt ggt gaa gat 762  
 Glu His His Leu Lys Glu Ser Leu Lys Gln Met Asn Val Gly Glu Asp  
 170 175 180 185

tta gaa aat gaa gat ttt gac agt cgt aga tac aaa ttt ttg gat gat 810  
 Leu Glu Asn Glu Asp Phe Asp Ser Arg Arg Tyr Lys Phe Leu Asp Asp  
 190 195 200

gat gga tcc att tct cct att gag gag tca aca gca gag gat gag gat 858  
 Asp Gly Ser Ile Ser Pro Ile Glu Glu Ser Thr Ala Glu Asp Glu Asp  
 205 210 215

gca aca cat ctt gaa gat aac gaa tgt gat atc aaa ttg gca ggg gat 906  
 Ala Thr His Leu Glu Asp Asn Glu Cys Asp Ile Lys Leu Ala Gly Asp  
 220 225 230

agt ttc ata gta agt tct gaa ttc cct gta aga ctg agt gta tac tta 954  
 Ser Phe Ile Val Ser Ser Glu Phe Pro Val Arg Leu Ser Val Tyr Leu  
 235 240 245

gaa gaa gag gat att act gaa gaa gct gct ttg tct aaa aag aga gct 1002  
 Glu Glu Glu Asp Ile Thr Glu Glu Ala Ala Leu Ser Lys Lys Arg Ala  
 250 255 260 265

aca aaa gcc aaa aat act gga cag aga ggc ctg aaa atg tga 1044  
 Thr Lys Ala Lys Asn Thr Gly Gln Arg Gly Leu Lys Met  
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caggatcatg aatgtcaaag gtgaagcata tagaaaaaac gacttcatag aaatgaataa 1104

agataaatgt ggatat 1120

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 <213> Homo sapiens

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 Lys Thr Gln Cys Ile Pro Tyr Ser Pro Lys Gly Glu Lys Arg Asn Pro  
 35 40 45  
 Ile Arg Lys Phe Val Arg Thr Pro Glu Ser Val His Ala Ser Asp Ser  
 50 55 60  
 Ser Ser Asp Ser Ser Phe Glu Pro Ile Pro Leu Thr Ile Lys Ala Ile

65 70 75 80  
Phe Glu Arg Phe Lys Asn Arg Lys Lys Arg Tyr Lys Lys Lys Lys Lys  
85 90 95  
Arg Arg Tyr Gln Pro Thr Gly Arg Pro Arg Gly Arg Pro Glu Gly Arg  
100 105 110  
Arg Asn Pro Ile Tyr Ser Leu Ile Asp Lys Lys Lys Gln Phe Arg Ser  
115 120 125  
Arg Gly Ser Gly Phe Pro Phe Leu Glu Ser Glu Asn Glu Lys Asn Ala  
130 135 140  
Pro Trp Arg Lys Ile Leu Thr Phe Glu Gln Ala Val Ala Arg Gly Phe  
145 150 155 160  
Phe Asn Tyr Ile Glu Lys Leu Lys Tyr Glu His His Leu Lys Glu Ser  
165 170 175  
Leu Lys Gln Met Asn Val Gly Glu Asp Leu Glu Asn Glu Asp Phe Asp  
180 185 190  
Ser Arg Arg Tyr Lys Phe Leu Asp Asp Asp Gly Ser Ile Ser Pro Ile  
195 200 205  
Glu Glu Ser Thr Ala Glu Asp Glu Asp Ala Thr His Leu Glu Asp Asn  
210 215 220  
Glu Cys Asp Ile Lys Leu Ala Gly Asp Ser Phe Ile Val Ser Ser Glu  
225 230 235 240  
Phe Pro Val Arg Leu Ser Val Tyr Leu Glu Glu Glu Asp Ile Thr Glu  
245 250 255  
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260 265 270  
Gln Arg Gly Leu Lys Met  
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Arg Thr Leu Pro Gly Pro Ser Trp Val Arg Gly Ser Gly Pro Ser Val  
10 15 20 25

ctg agc cgc ctg cag gac gcg gcc gtg gtg cgg cct ggc ttc ctg agc 149  
Leu Ser Arg Leu Gln Asp Ala Ala Val Val Arg Pro Gly Phe Leu Ser  
30 35 40

acg gca gag gag gag acg ctg agc cga gaa ctg gag ccc gag ctg cgc 197  
Thr Ala Glu Glu Glu Thr Leu Ser Arg Glu Leu Glu Pro Glu Leu Arg  
45 50 55

cgc cgc cgc tac gaa tac gat cac tgg gac gcg gcc atc cac ggc ttc 245  
Arg Arg Arg Tyr Glu Tyr Asp His Trp Asp Ala Ala Ile His Gly Phe

05890668.092701

60	65	70	
cga gag aca gag aag tcg cgc tgg tca gaa gcc agc cgg gcc atc ctg			293
Arg Glu Thr Glu Lys Ser Arg Trp Ser Glu Ala Ser Arg Ala Ile Leu	80	85	
75			
cag cgc gtg cag gcg gcc gcc ttt ggc ccc ggc cag acc ctg ctc tcc			341
Gln Arg Val Gln Ala Ala Ala Phe Gly Pro Gly Gln Thr Leu Leu Ser	95	100	105
90			
tcc gtg cac gtg ctg gac ctg gaa gcc cgc ggc tac atc aag ccc cac			389
Ser Val His Val Leu Asp Leu Glu Ala Arg Gly Tyr Ile Lys Pro His	110	115	120
gtg gac agc atc aag ttc tgc ggg gcc acc atc gcc ggc ctg tct ctc			437
Val Asp Ser Ile Lys Phe Cys Gly Ala Thr Ile Ala Gly Leu Ser Leu	125	130	135
ctg tct ccc agc gtt atg cgg ctg gtg cac acc cag gag ccg ggg gag			485
Leu Ser Pro Ser Val Met Arg Leu Val His Thr Gln Glu Pro Gly Glu	140	145	150
tgg ctg gaa ctc ttg ctg gag ccg ggc tcc ctc tac atc ctt agg ggc			533
Trp Leu Glu Leu Leu Leu Glu Pro Gly Ser Leu Tyr Ile Leu Arg Gly	155	160	165
tca gcc cgt tat gac ttc tcc cat gag atc ctt cgg gat gaa gag tcc			581
Ser Ala Arg Tyr Asp Phe Ser His Glu Ile Leu Arg Asp Glu Glu Ser	170	175	180
			185
ttc ttt ggg gaa cgc cgg att ccc cgg ggc cgg cgc atc tcc gtg atc			629
Phe Phe Gly Glu Arg Arg Ile Pro Arg Gly Arg Arg Ile Ser Val Ile	190	195	200
tgc cgc tcc ctc cct gag ggc atg ggg cca ggg gag tct gga cag ccg			677
Cys Arg Ser Leu Pro Glu Gly Met Gly Pro Gly Glu Ser Gly Gln Pro	205	210	215
ccc cca gcc tgc tga cccccagctt tctacagaca ccagatttgt gaataaagtt			732
Pro Pro Ala Cys			
220			
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<210> 158  
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 <212> PRT  
 <213> Homo sapiens

<400> 158  
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 Ala Val Val Arg Pro Gly Phe Leu Ser Thr Ala Glu Glu Glu Thr Leu  
 35 40 45

09090600 092701

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Ser Arg Glu Leu Glu Pro Glu Leu Arg Arg Arg Arg Tyr Glu Tyr Asp
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His Trp Asp Ala Ala Ile His Gly Phe Arg Glu Thr Glu Lys Ser Arg
 65          70          75          80
Trp Ser Glu Ala Ser Arg Ala Ile Leu Gln Arg Val Gln Ala Ala Ala
          85          90          95
Phe Gly Pro Gly Gln Thr Leu Leu Ser Ser Val His Val Leu Asp Leu
          100          105          110
Glu Ala Arg Gly Tyr Ile Lys Pro His Val Asp Ser Ile Lys Phe Cys
          115          120          125
Gly Ala Thr Ile Ala Gly Leu Ser Leu Leu Ser Pro Ser Val Met Arg
          130          135          140
Leu Val His Thr Gln Glu Pro Gly Glu Trp Leu Glu Leu Leu Leu Glu
145          150          155          160
Pro Gly Ser Leu Tyr Ile Leu Arg Gly Ser Ala Arg Tyr Asp Phe Ser
          165          170          175
His Glu Ile Leu Arg Asp Glu Glu Ser Phe Phe Gly Glu Arg Arg Ile
          180          185          190
Pro Arg Gly Arg Arg Ile Ser Val Ile Cys Arg Ser Leu Pro Glu Gly
          195          200          205
Met Gly Pro Gly Glu Ser Gly Gln Pro Pro Pro Ala Cys
          210          215          220

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<210> 159  
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<220>  
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                                Met Lys Lys Phe Phe Gln Glu
                                1                                5

ttc aag gcc gac atc aag ttc aaa agc gcg gga ccc ggt cag aag ctc 163
Phe Lys Ala Asp Ile Lys Phe Lys Ser Ala Gly Pro Gly Gln Lys Leu
          10          15          20

aaa gag tcc gtg ggg gaa aag gcc cac aaa gag aag ccc aac cag cca 211
Lys Glu Ser Val Gly Glu Lys Ala His Lys Glu Lys Pro Asn Gln Pro
          25          30          35

gcc ccc agg ccg ccc cgc cag gga ccc acc aat gag gca cag atg gca 259
Ala Pro Arg Pro Pro Arg Gln Gly Pro Thr Asn Glu Ala Gln Met Ala
          40          45          50          55

gcc gct gcc gcc cta gcc cgg ctg gag cag aag cag tcc cgg gcc tgg 307
Ala Ala Ala Ala Leu Ala Arg Leu Glu Gln Lys Gln Ser Arg Ala Trp
          60          65          70

ggc ccc aca tcg cag gac acc atc cga aac cag gtg aga aag gaa ctt 355

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Gly	Pro	Thr	Ser	Gln	Asp	Thr	Ile	Arg	Asn	Gln	Val	Arg	Lys	Glu	Leu		
			75					80					85				
caa	gcc	gaa	gcc	acc	gtc	agc	ggg	agc	ccc	gag	gcc	cca	ggg	acc	aac	403	
Gln	Ala	Glu	Ala	Thr	Val	Ser	Gly	Ser	Pro	Glu	Ala	Pro	Gly	Thr	Asn		
		90					95					100					
gtg	gta	tct	gag	ccc	aga	gag	gaa	ggc	tct	gcc	cac	ctg	gct	gtg	cct	451	
Val	Val	Ser	Glu	Pro	Arg	Glu	Glu	Gly	Ser	Ala	His	Leu	Ala	Val	Pro		
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ggc	gtg	tac	ttc	acc	tgt	ccg	ctc	act	ggg	gcc	acc	ctg	agg	aag	gac	499	
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cag	cgg	gac	gcc	tgc	atc	aag	gag	gcc	att	ctc	ttg	cac	ttc	tcc	acc	547	
Gln	Arg	Asp	Ala	Cys	Ile	Lys	Glu	Ala	Ile	Leu	Leu	His	Phe	Ser	Thr		
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Asp	Pro	Val	Ala	Ala	Ser	Ile	Met	Lys	Ile	Tyr	Thr	Phe	Asn	Lys	Asp		
			155					160					165				
cag	gac	cgg	gtg	aag	ctg	ggt	gtg	gac	acc	att	gcc	aag	tac	ctg	gac	643	
Gln	Asp	Arg	Val	Lys	Leu	Gly	Val	Asp	Thr	Ile	Ala	Lys	Tyr	Leu	Asp		
			170				175					180					
aac	atc	cac	ctg	cac	ccc	gag	gag	gag	aag	tac	cgg	aag	atc	aag	ctg	691	
Asn	Ile	His	Leu	His	Pro	Glu	Glu	Glu	Lys	Tyr	Arg	Lys	Ile	Lys	Leu		
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Gln	Asn	Lys	Val	Phe	Gln	Glu	Arg	Ile	Asn	Cys	Leu	Glu	Gly	Thr	His		
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Glu	Phe	Phe	Glu	Ala	Ile	Gly	Phe	Gln	Lys	Val	Leu	Leu	Pro	Ala	Gln		
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Ala	Gln	Pro	Gln	Ser	Leu	Glu	Arg	His	Lys	Glu	Gln	Leu	Leu	Ala	Ala		
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Glu	Pro	Val	Arg	Ala	Lys	Leu	Asp	Arg	Gln	Arg	Arg	Val	Phe	Gln	Pro		
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Ser	Pro	Leu	Ala	Ser	Gln	Phe	Glu	Leu	Pro	Gly	Asp	Phe	Phe	Asn	Leu		
					285					290					295		
aca	gca	gag	gag	atc	aag	cgg	gag	cag	agg	ctc	agg	tcc	gag	gcg	gtg	1027	
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cct ttt gag ctg ctg gcc tcg gga ggg cag aag ctg tcc gag gac gag Pro Phe Glu Leu Leu Ala Ser Gly Gly Gln Lys Leu Ser Glu Asp Glu 380 385 390			1267
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Thr Asn Glu Ala Gln Met Ala Ala Ala Leu Ala Arg Leu Glu 50 55 60
Gln Lys Gln Ser Arg Ala Trp Gly Pro Thr Ser Gln Asp Thr Ile Arg 65 70 75 80
Asn Gln Val Arg Lys Glu Leu Gln Ala Glu Ala Thr Val Ser Gly Ser 85 90 95



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Pro Glu Ala Pro Gly Thr Asn Val Val Ser Glu Pro Arg Glu Glu Gly  
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 Ser Ala His Leu Ala Val Pro Gly Val Tyr Phe Thr Cys Pro Leu Thr  
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 Gly Ala Thr Leu Arg Lys Asp Gln Arg Asp Ala Cys Ile Lys Glu Ala  
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 Ile Leu Leu His Phe Ser Thr Asp Pro Val Ala Ala Ser Ile Met Lys  
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 Ile Tyr Thr Phe Asn Lys Asp Gln Asp Arg Val Lys Leu Gly Val Asp  
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 Thr Ile Ala Lys Tyr Leu Asp Asn Ile His Leu His Pro Glu Glu Glu  
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 Lys Tyr Arg Lys Ile Lys Leu Gln Asn Lys Val Phe Gln Glu Arg Ile  
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 Asn Cys Leu Glu Gly Thr His Glu Phe Phe Glu Ala Ile Gly Phe Gln  
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 Lys Val Leu Leu Pro Ala Gln Asp Gln Glu Asp Pro Glu Glu Phe Tyr  
 225 230 235 240  
 Val Leu Ser Glu Thr Thr Leu Ala Gln Pro Gln Ser Leu Glu Arg His  
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 Lys Glu Gln Leu Leu Ala Ala Glu Pro Val Arg Ala Lys Leu Asp Arg  
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 Gln Arg Arg Val Phe Gln Pro Ser Pro Leu Ala Ser Gln Phe Glu Leu  
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 Pro Gly Asp Phe Phe Asn Leu Thr Ala Glu Glu Ile Lys Arg Glu Gln  
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 Ala Met Arg Glu Lys Glu Glu Gln Arg Gly Leu Arg Lys Tyr Asn Tyr  
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 Asp Ile Lys Ala Ala Gly Ala Glu Pro Asp Ser Ile Leu Lys Pro Glu  
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